

L Number	Hits	Search Text	DB	Time stamp
1	6	cory NEAR suzanne	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:36
2	107	bcl NEAR w	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:34
3	4	"5789201"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:34
4	2	"5883229"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:34
11	6	Guastella NEAR John	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:35
12	2	Holmgreen NEAR Shaun	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:37
15	97	(bcl NEAR w) and apoptosis	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:38
16	28	((bcl NEAR w) and apoptosis) and bcl\$3.clm.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:39
17	8	bcl-w.clm.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/03/29 14:40
18	10	(US-5883229-\$ or US-5789201-\$).did. or (US-20020119943-\$ or US-20040014218-\$).did. or (WO-9735971-\$ or WO-9914321-\$ or WO-9913710-\$ or WO-9115116-\$).did. or (WO-9913710-\$ or US-20020119943-\$).did.	USPAT; US-PGPUB; EPO; DERWENT	2004/03/29 14:40

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(FILE 'HOME' ENTERED AT 14:41:41 ON 29 MAR 2004)

FILE 'MEDLINE, CANCERLIT, SCISEARCH, CAPLUS' ENTERED AT 14:42:01 ON 29 MAR 2004

E CORY S?/AU
L1 124 S E11
L2 416 S E1
L3 540 S L1 OR L2
L4 186 S L3 AND BCL?
L5 29 S L4 AND BCL-W
L6 10 DUP REM L5 (19 DUPLICATES REMOVED)
L7 10 SORT L6 PY
L8 79913 S BCL?
L9 318 S L8 AND BCL-W
L10 16 S L9 AND PY<=1997
L11 6 DUP REM L10 (10 DUPLICATES REMOVED)
L12 6 SORT L11 PY

=> d an ti so au ab pi l7 3 8 1 4 7 9

L7 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:650444 CAPLUS
DN 127:327462
TI A novel mammalian gene, **bcl-w**, belongs to the
bcl-2 family of apoptosis-controlling genes
SO PCT Int. Appl., 85 pp.
CODEN: PIXXD2
IN **Cory, Suzanne**; Adams, Jerry McKee; Gibson, Leonie M.; Holmgreen,
Shaun P.
AB Human and mouse cDNAs for **bcl-2**-related gene **bcl-w**
and the corresponding proteins are disclosed. The present
invention is broadly directed to therapeutic mols. capable of inter alia
modulating apoptosis in mammalian cells. The therapeutic mols. of the
present invention encompass genetic sequences and chemical entities capable
of regulating expression of **bcl-w** family and which
promotes cell survival. The therapeutic mols. of the present invention
may have further utility in delaying cell cycle entry. In addition, the
present invention extends to chemical entities capable of modulating activity
and function of the translation product of the **bcl-w**
gene. The present invention also extends to the translation product of
the **bcl-w** gene and its use in, for example, therapy,
diagnosis, antibody generation and, as a screening tool for therapeutic
mols. capable of modulating physiol. cell death or survival and/or
modulating cell cycle entry. The **bcl-w** gene was
mapped to human chromosome 14q11.2. Alternative splicing of the
bcl-w gene transcript produced an mRNA for a **bcl**
-w-rox chimera. The **bcl-w** gene was
expressed in many cell types. Amongst the tissues surveyed, the level was
highest in brain, colon and salivary gland. A survey of 50 mouse
hemopoietic cell lines revealed that **bcl-w** expression
was common in cells of several myeloid lineages, including macrophage,
megakaryocyte, erythroid and mast cell lines, but rare in either B or T
lymphoid lines.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 9735971	A1	19971002	WO 1997-AU199	19970327
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
CA 2250207	AA	19971002	CA 1997-2250207	19970327
AU 9721439	A1	19971017	AU 1997-21439	19970327
AU 728863	B2	20010118		

STN: SEARCH HISTORY

EP 932674 A1 19990804 EP 1997-913986 19970327
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO
 JP 2000513566 T2 20001017 JP 1997-533874 19970327
 US 2002119943 A1 20020829 US 2001-925674 20010809

L7 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:215553 CAPLUS

DN 130:235990

TI Animals carrying **bcl-w** mutations and their use in the study of male infertility

SO PCT Int. Appl., 52 pp.

CODEN: PIXXD2

IN **Cory, Suzanne**; Adams, Jerry; Print, Cris; Gibson, Leonie; Koentgen, Frank

AB Transgenic mice carrying a disruption of the **bcl-w** gene or of genes interacting with it and that fail to undergo productive spermatogenesis and are male infertile are described for use in studies of male fertility and of the biol. role of **bcl-w**. Such animals can be used to screen for therapeutic mols. including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in said animals as well as a model for mols. and genetic sequences which can induce infertility. The **bcl-w** gene was disrupted by insertional inactivation. Inactivation of **bcl-w** did not affect survival of fetal and neonatal mice and the mutation showed a near-normal Mendelian segregation. Hematopoiesis was unaffected by the mutation but the testes showed heterogeneous pathol. changes in the seminiferous tubules. Sertoli cells remained normal although low in number and Leydig cell were increased by 50%. Germ cell nos. declined steadily with as the stage of development advanced. The mutation did not affect androgen levels or androgen responses in other organs.

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9913710	A1	19990325	WO 1998-AU764	19980916
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	CA 2304132	AA	19990325	CA 1998-2304132	19980916
	AU 9890557	A1	19990405	AU 1998-90557	19980916
	AU 757728	B2	20030306		
	EP 1011319	A1	20000628	EP 1998-942391	19980916
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L7 ANSWER 1 OF 10 MEDLINE on STN

AN 96358615 MEDLINE

TI **bcl-w**, a novel member of the **bcl-2** family, promotes cell survival.

SO Oncogene, (1996 Aug 15) 13 (4) 665-75.

Journal code: 8711562. ISSN: 0950-9232.

AU Gibson L; Holmgreen S P; Huang D C; Bernard O; Copeland N G; Jenkins N A; Sutherland G R; Baker E; Adams J M; **Cory S**

AB The prototypic mammalian regulator of cell death is **bcl-2**, the oncogene implicated in the development of human follicular lymphoma. Several homologues of **bcl-2** are now known. Using a PCR-based strategy we cloned a novel member of this gene family, denoted **bcl-w**. The gene, which is highly conserved between mouse and human, resides near the T-cell antigen receptor alpha gene within the central portion of mouse chromosome 14 and on human chromosome 14 at band q11. Enforced expression of **bcl-w** rendered lymphoid and myeloid cells refractory to several (but not all) cytotoxic conditions. Thus, like **Bcl-2** and **Bcl-x**, the **Bcl-w** protein promotes cell survival, in contrast to

other close homologues, Bax and Bak, which facilitate cell death. Comparison of the expected amino acid sequence of **Bcl-w** with that of these relatives helps to delineate residues likely to convey survival or anti-survival function. While expression of **bcl-w** was uncommon in B or T lymphoid cell lines, the mRNA was observed in almost all murine myeloid cell lines analysed and in a wide range of tissues. These findings suggest that **bcl-w** participates in the control of apoptosis in multiple cell types. Its functional similarity to **bcl-2** also makes it an attractive candidate proto-oncogene.

L7 ANSWER 4 OF 10 MEDLINE on STN
 AN 1998445387 MEDLINE
 TI Apoptosis regulator **bcl-w** is essential for spermatogenesis but appears otherwise redundant.
 SO Proceedings of the National Academy of Sciences of the United States of America, (1998 Oct 13) 95 (21) 12424-31.
 Journal code: 7505876. ISSN: 0027-8424.
 AU Print C G; Loveland K L; Gibson L; Meehan T; Stylianou A; Wreford N; de Kretser D; Metcalf D; Kontgen F; Adams J M; **Cory S**
 AB Proteins of the **Bcl-2** family are important regulators of apoptosis in many tissues of the embryo and adult. The recently isolated **bcl-w** gene encodes a pro-survival member of the **Bcl-2** family, which is widely expressed. To explore its physiological role, we have inactivated the **bcl-w** gene in the mouse by homologous recombination. Mice that lack **Bcl-w** were viable, healthy, and normal in appearance. Most tissues exhibited typical histology, and hematopoiesis was unaffected, presumably due to redundant function with other pro-survival family members. Although female reproductive function was normal, the males were infertile. The testes developed normally, and the initial, prepubertal wave of spermatogenesis was largely unaffected. The seminiferous tubules of adult males, however, were disorganized, contained numerous apoptotic cells, and produced no mature sperm. Both Sertoli cells and germ cells of all types were reduced in number, the most mature germ cells being the most severely depleted. The **bcl-w**^{-/-} mouse provides a unique model of failed spermatogenesis in the adult that may be relevant to some cases of human male sterility.

L7 ANSWER 7 OF 10 MEDLINE on STN
 AN 1999310955 MEDLINE
 TI Survival activity of **Bcl-2** homologs **Bcl-w** and A1 only partially correlates with their ability to bind pro-apoptotic family members.
 SO Cell death and differentiation, (1999 Jun) 6 (6) 525-32.
 Journal code: 9437445. ISSN: 1350-9047.
 AU Holmgren S P; Huang D C; Adams J M; **Cory S**
 AB Certain **Bcl-2** family members promote cell survival, whereas others promote apoptosis. To explore further how heterodimerization of opposing members affects survival activity, we have compared the abilities of the anti-apoptotic **Bcl-w** and A1 to bind to the pro-apoptotic Bax, Bak, Bad and Bik and to protect cells from their cytotoxic action. **Bcl-w** co-immunoprecipitated from cell lysates with Bax, Bak, Bad and Bik, but A1 bound only Bak and Bik. Mutation of A1 at a highly conserved glycine within the BH1 domain prevented binding, but the comparable **Bcl-w** mutant still bound Bak, Bad and Bik, indicating that the glycine is not essential for all heterodimerization. **Bcl-w** and A1 protected against apoptosis induced by over-expression of Bax or Bad but not that induced by Bak or Bik. With several gene pairs, binding and protection were discordant. The results may reflect critical threshold affinities but also suggest that certain pro-apoptotic proteins may also contribute to apoptosis by a mechanism independent of binding pro-survival proteins.

L7 ANSWER 9 OF 10 MEDLINE on STN
 AN 2001360165 MEDLINE
 TI Tissue expression and subcellular localization of the pro-survival molecule **Bcl-w**.
 SO Cell death and differentiation, (2001 May) 8 (5) 486-94.

Journal code: 9437445. ISSN: 1350-9047.

AU O'Reilly L A; Print C; Hausmann G; Moriishi K; Cory S; Huang D
C; Strasser A

AB Anti-apoptotic members of the Bcl-2 family, such as Bcl-w, maintain cell viability by preventing the activation of the cell death effectors, the caspases. Gene targeting experiments in mice have demonstrated that Bcl-w is required for spermatogenesis and for survival of damaged epithelial cells in the gut. Bcl-w is, however, dispensable for physiological cell death in other tissues. Here we report on the analysis of Bcl-w protein expression using a panel of novel monoclonal antibodies. Bcl-w is found in a diverse range of tissues including colon, brain and testes. A survey of transformed cell lines and purified hematopoietic cells demonstrated that Bcl-w is expressed in cells of myeloid, lymphoid and epithelial origin. Subcellular fractionation and confocal laser scanning microscopy demonstrated that Bcl-w protein is associated with intracellular membranes. The implications of these results are discussed in the context of the phenotype of Bcl-w-null mice and recent data that suggest that Bcl-w may play a role in colon carcinogenesis.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:01:08 ; Search time 2762.74 seconds

(without alignments)
9146.355 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION Sequence 6 from Patent EP0932674.

ACCESSION AX022529

VERSION AX022529.1 GI:10046125

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 Adams J M., Holmgren S. P., Cory S. and Gibson L. M.

A novel mammalian gene, bcl-2, belongs to the bcl-2 family of

apoptosis-controlling genes

Patent: EP 0932674-A 6 04-AUG-1999;

JOURNAL

AMRAD OPERATIONS PTY LTD (AU) Location/Qualifiers

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VERSION AX030817.1 GI:10278311
KEYWORDS
SOURCE unidentified
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REFERENCE
1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-2, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU) ; HOLMGREN SHAWN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)

FEATURES source

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ORIGIN

Query Match 100.0%; Score 583; DB 6; Length 583;
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QY 421 AGTGGGGGCTGGGCGAGTTCAAGCTCTATAAGGGGAGCGGGCCCTGAGAGAGCGGG 480
DB 421 AGTGGGGGCTGGGCGAGTTCAAGCTCTATAAGGGGAGCGGGCCCTGAGAGAGCGGG 480
QY 481 CGTCTGCGGAGGAGGAAGTGGGCAATGAGAGCAAGTCTGACCGGGGCGCTGACACTG 540
DB 481 CGTCTGCGGAGGAGGAAGTGGGCAATGAGAGCAAGTCTGACCGGGGCGCTGACACTG 540
QY 541 GGGGCGCTGTGTAAGTGTGGGCTTTTGTCTAGCAAGTGAA 583
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RESULT 3
AX481423 582 bp DNA linear PAT 16-AUG-2002
LOCUS AX481423
DEFINITION Sequence 37 from Patent WO02055693.

ACCESSION AX481423
 VERSION AX481423.1 GI:22316337
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Kreutzer, R., Jilmer, S., Post, S. and Hadwiger, P.
 Method for inhibiting the expression of a target gene
 Parent: WO 02055693-A 37 18-UTR-2002;
 JOURNAL Ribopharma AG (DE)

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ORIGIN
 Query Match 99.0%; Score 577.2; DB 6; Length 582;
 Best Local Similarity 99.5%; Pred. No. 4.8e-120;
 Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ATGGCGACCCGAGCTCGGCCCAAGACACAGGGCTCTGTGCGAGACTTTGATAGTTAT 60
DB 1 ATGGCGACCCGAGCTCGGCCCAAGACACAGGGCTCTGTGCGAGACTTTGATAGTTAT 60
QY 61 AAGCTGAGGCGAAGAGGTTATCTGTGAGACTGCCCCGGGAGAGGCCCAAGACTGAC 120
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QY 181 TTCTCTGATCTGGGCGCTCAGCTCATGTGACCCCAAGCTCAGCCCAAGACGCTTACC 240
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QY 241 CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCCCACTGGGGCGCTTGTAGCTTCTTT 300
DB 241 CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCCCACTGGGGCGCTTGTAGCTTCTTT 300
QY 301 CTCTTTGGGGCTGACATGTGTGTGAGAGTGTCAACAGAGATGAGAACCACTGTGTGGA 360
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DB 481 CGTCTGCGGAGGAGGAACTGGGCAATCAGTGAAGACAGTGTGACGGGGGCGGTGTGAC 540
QY 541 GGGGGCCCTGTGTAAGTGAAGGGGCTTTTGTGCTAGCAAGTGA 582
DB 541 GGGGGCCCTGTGTAAGTGAAGGGGCTTTTGTGCTAGCAAGTGA 582
  
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RESULT 4
 HSU59747 582 bp mRNA linear PRI 29-SEP-1996
 LOCUS HSU59747
 DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
 ACCESSION U59747
 VERSION U59747.1 GI:1572492
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 582)
 Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)

JOURNAL MEDLINE
 PUBMED 96358615
 8761287
 2 (bases 1 to 582)
 Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and Cory, S.

AUTHORS
 Direct Submission
 Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia

FEATURES
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 /codon_start=1
 /product="Bcl-w"
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 /db_xref="GI:1572492"
 /translation="MATSASAPDTRALVADVRYKLRKGYVCGAREPRAADPLHQAMRAQDEFEFRFRFTSDLAQLHVTGSAQDRFTQVSDLPQSGPWWGLVAFVFGALCAESVNMKEPVLGVQVEMVVALETFLADWIHSSGMAEFTALYGDALBEARLRRENMASVRLTGAVALGALVTVGAFASK"

ORIGIN
 Query Match 99.0%; Score 577.2; DB 9; Length 582;
 Best Local Similarity 99.5%; Pred. No. 4.8e-120;
 Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 ATGGGAGACCCGAGCTCGGCCCAAGACACAGGGGCTCTGTGCGAGACTTTGATAGTTAT 60
QY 61 AAGCTGAGGCGAAGAGGTTATCTGTGAGACTGCCCCGGGAGAGGCCCAAGACTGAC 120
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QY 121 CCGCTGACACCAAGGCATCGGGGCACTGGAGATGATGATGACCCGCTCCGGCGAC 180
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QY 241 CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCCCACTGGGGCGCTTGTAGCTTCTTT 300
DB 241 CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCCCACTGGGGCGCTTGTAGCTTCTTT 300
QY 301 CTCTTTGGGGCTGACATGTGTGTGAGAGTGTCAACAGAGATGAGAACCACTGTGTGGA 360
DB 301 CTCTTTGGGGCTGACATGTGTGTGAGAGTGTCAACAGAGATGAGAACCACTGTGTGGA 360
QY 361 CAAATGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 361 CAAATGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 421 AGTGGGGGCTGGGCGAGTTCAAGCTCTATACGGGACCGGGGCGCTTGTGAGAGAGCGCG 480
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DB 481 CCGTCTGCGGAGGAGGAACTGAGCATCACTGAGGACAGTCTGACGGGGCCGTGGCACTG 540
QY 541 GGGGCGCCCTGTACTGTAGTGGGCGCTTTTGTGTAGCACTGA 582
DB 541 GGGGCGCCCTGTACTGTAGTGGGCGCTTTTGTGTAGCACTGA 582

RESULT 5
DB461 3542 bp mRNA linear PRI 06-OCT-2001
LOCUS Human mRNA for KIAA0271 gene, complete cds.
DEFINITION DB461
ACCESSION DB461.1 GI:1944417
VERSION KIAA0271.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y., Chata,O., Tanaka,A., Kocani,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain
JOURNAL DNA Res. 3 (5), 321-329 (1996)
MEDLINE 97191544
PUBMED 9039502
REFERENCE 2 (bases 1 to 3542)
AUTHORS Chata,O., Nagase,T., Kikuno,R. and Nomura,N.
TITLE Direct Submission
SUBMITTED (27-AUG-1996) Osamu Chata, Kazusa DNA Research Institute, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
JOURNAL (E-mail:cdna@kzusa.or.jp, Tel:+81-438-52-3913)
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ORIGIN
Query Match 98.6%; Score 575; DB 9; Length 3542;
Best Local Similarity 99.1%; Pred. No. 1.2e-119;
Matches 576; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGACCTCGGCCCAACACACACGGGCTCTGTGGCAGACTTTGTAGTAT 60
DB 177 ATGGCGACCCCGACCTCGGCCCAACACACACGGGCTCTGTGGCAGACTTTGTAGTAT 236
QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGCCACAGCAGCTGAC 120
DB 237 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGCCACAGCAGCTGAC 296

QY 121 CCGCTCACCAAGCCATGCGGGAGCTGGAGATGAGTTGGAGACCCCGCTTCGGGGAC 180
DB 297 CCGCTCACCAAGCCATGCGGGAGCTGGAGATGAGTTGGAGACCCCGCTTCGGGGAC 356
QY 181 TTCTGTGATCTGGCGGCTAGCTGATGATGACCCCAAGGCTCAGCCAGCAAGCTTACC 240
DB 357 TTCTGTGATCTGGCGGCTAGCTGATGATGACCCCAAGGCTCAGCCAGCAAGCTTACC 416
QY 241 CAGTCTCCGACCAACTTTTTCAGGGGGCCCAACTGCGGGCGCGCTTGTAGCTTTCTT 300
DB 417 CAGTCTCCGACCAACTTTTTCAGGGGGCCCAACTGCGGGCGCGCTTGTAGCTTTCTT 476
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QY 361 CAGTGCAGAGATGATGTGTGCTTCTCTGAGACGCGGCTGTGACTGATCCACAGC 420
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QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTTATACGGGAGACGGGGCCCTGAGAGAGCGCG 480
DB 597 AGTGGGGGCTGGCGGAGTTCAAGCTTATACGGGAGACGGGGCCCTGAGAGAGCGCG 656
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DB 657 CCGTCTGCGGAGGGGAACTGGGATCAGTGAAGACAGTGTGAACGGGGGCGCTGGCACTG 716
QY 541 GGGGCGCCCTGTACTGTAGGCGGCTTTTGTCTAGCAAGTGA 583
DB 717 GGGGCGCCCTGTACTGTAGGCGGCTTTTGTCTAGCAAGTGA 759

RESULT 6
AR020780 579 bp DNA linear PAT 05-DEC-1998
LOCUS AR020780
DEFINITION Sequence 2 from patent US 5789201.
ACCESSION AR020780
VERSION AR020780.1 GI:3975395
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 579)
AUTHORS Giastrella,J.
TITLE Gene coding for bcl-y a bcl-2 homologue
JOURNAL Patent: US 5789201-A 2 04-AUG-1998;
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ORIGIN
Query Match 97.4%; Score 567.8; DB 6; Length 579;
Best Local Similarity 98.8%; Pred. No. 6.4e-118;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 121 CCACTGACCAAGCAATGCGGGAGCTGAGATGAGTTGAGACCGCGCTTCGCGCGCAC 180
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QY 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTAGGCAAG 579
Db 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTAGGCAAG 579

RESULT 7
AF096291 582 bp mRNA linear ROD 28-FEB-2000

LOCUS AF096291 Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
DEFINITION AF096291.1 GI:3747129
VERSION AF096291.1 GI:3747129
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 582)
AUTHORS Hammer, S., Skoglova, Y. and Lindholm, D.
TITLE Differential expression of bcl-w and bcl-x messenger RNA in the
JOURNAL Neurosciences 91 (2), 673-684 (1999)
MEDLINE 98292146
PUBMED 10366024

REFERENCE 2 (bases 1 to 582)
AUTHORS Hammer, S., Skoglova, Y. and Lindholm, D.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
University, Box 587, BMC, Uppsala 751 23, Sweden
Location/Qualifiers

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Query Match 90.5%; Score 527.6; DB 10; Length 582;
Best Local Similarity 94.2%; Pred. No. 7.7e-109;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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QY 61 AAGCTGAGCAGAAAGGTTATGTGTGAGCTGAGCCCGGGAGAGGCCCAAGAGCTGAC 120
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Db 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCTTTCTT 300
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QY 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTAGGCAAG 582
Db 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTAGGCAAG 582

RESULT 8
AY185100 1110 bp mRNA linear ROD 24-JUN-2003
LOCUS AY185100 Rattus norvegicus BCL-WEL mRNA, complete cds.
DEFINITION AY185100
ACCESSION AY185100.1 GI:32185284
VERSION AY185100.1 GI:32185284
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1110)
AUTHORS Itoh, T., Itoh, A. and Pleasure, D.
TITLE Bcl-2-related protein family gene expression during
JOURNAL oligodendroglial differentiation
MEDLINE U. Neurochem. 85 (6), 1500-1512 (2003)
PUBMED 12672518

REFERENCE 2 (bases 1 to 1110)
AUTHORS Itoh, T., Itoh, A. and Pleasure, D.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Neurology Research. The Children's Hospital
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
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CDS

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Query Match	90.5%;	Score 527.6;	DB 10;	Length 1110;
Best Local Similarity	94.2%;	Pred. No. 7.2e-109;		
Matches 548;	Conservative	0;	Mismatches 34;	Indels 0;
				Gaps 0;

CDS

AUTHORS	Itch, T., Itch, A. and Pleasure, D.
TITLE	Bcl-2-related protein family gene expression during oligodendroglial differentiation
JOURNAL	J. Neurochem. 85 (6), 1500-1512 (2003)
MEDLINE	22672518
PMID	12787069
REFERENCE	2 (bases 1 to 3487)
AUTHORS	Itch, T., Itch, A. and Pleasure, D.
TITLE	Direct Submission
JOURNAL	Submitted (21-NOV-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA
FEATURES	location/Qualifiers
source	1..3487

ORIGIN

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ORIGIN

Query Match	90.5%;	Score	527.6;	DB	10;	Length	3487;
Best Local Similarity	94.24;	Pred. No.	6.2e-109;				
Matches	548;	Conservative	0;	Mismatches	34;	Indels	0;
						Gaps	0;

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Db	170	ATGCGAACCCAGGCTCAACCCGAGACAGCGGCTTAAGTGCTGACTTTGTAGGCTAT	229
QY	61	AAGCTGAGGCGAAGAGGGTTATGTCTGTGAGACTGCGCCCGGGAGGGCCCAAGACGTGAC	120
Db	230	AAGCTGAGGCGAAGAGGGTTATGTCTGTGAGACTGCGCCCTGGGGAAAGGCCAGACCGGAC	289
QY	121	CCGCTGCACCAAGGCATCCGGGGAGCTGGAGATGATTCGAGACCCTCCGCGCAC	180
Db	290	CCGCTGCACCAAGGCATGCGGGAGCTGGAGACGAGTTTGAGACCCGCTTCGGCGCAC	349
QY	181	TTCTCTGATCTGGCGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAACGTTCA	240
Db	350	TTCTCTGATCTGGCGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAACGTTCA	300
QY	241	CAGGCTCTCCAGCAACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGAGCTTCTTT	300
Db	410	CAGGTTTCCAGCAACTTTTCCAGGGGGCCCCAACTGGGGCCGCTTGAGCTTCTTT	469
QY	301	CTCTTTGGGGCTGCACCTGTGTCTGAGAGTTCACCAAGAGAGATGGAACCACTGGTGG	360
Db	470	GCTTTTGGGGCTGCCTGTGTCTGAGAGTTCACCAAGAGAGATGGAACCACTGGTGG	529
QY	361	CAAGTGCAGAGTGGATGTGGCTTACCTGAGACGCGGCTGTGCACTGATCCACAGC	420
Db	530	CAAGTGCAGAGTGGATGTGATGACTTACCTGAGACACCGCTTGCTGATCTGATTCACAGC	589
QY	421	AGTGGGGGCTGGCGGAGTTCAACGCTTATACGGGGACGGGGCCCTTGAGAGAGCGGG	480
Db	590	AGTGGGGGCTGGCGGAGTTCAACGCTTATACGGGGACGGGGCCCTTGAGAGAGCGGG	649
QY	481	CGTCTGCGGAGAGGGAACTGGGCACTGATGAGACAGTGTGAGCGGGGGCCGTGGCACTG	540
Db	650	CGTCTGCGGAGAGGGAACTGGGCACTGATGAGAGCAGTGTGAGCGGGGGCTGTGGCACTG	709
QY	541	GGGGGCTCTGTAACGTGAGGGGCTTTTGTGATGACAGTGA 582	
Db	710	GGGGGCTCTGTACTGTGAGGGGCTTTTGTGATGACAGTGA 751	

ORIGIN	FEATURES
<p>Query Match 89.7%; Score 522.8; DB 10; Length 582; Best Local Similarity 93.6%; Pred. No. 9.4e-108; Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;</p>	<p>SOURCE Mus musculus (house mouse)</p> <p>ORGANISM Mus musculus</p> <p>REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathia; Muridae; Murinae; Mus. 1 (bases 1 to 582)</p> <p>AUTHORS Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-2, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)</p> <p>JOURNAL Oncogene 13 (4), 665-675 (1996)</p> <p>MEDLINE 9638615</p> <p>PUBMED 8761287</p> <p>REFERENCES 2 (bases 1 to 582) Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Adams, J.M. and Cory, S. Direct Submission Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia</p> <p>FEATURES source 1..582 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /chromosome="14" /cell_line="Baf3" 1..582 /gene="bcl-w" 1..582 /gene="bcl-w" /notes="promotes cell survival; Bcl-2 homolog" /codon_start=1 /product="Bcl-w" /protein_id="AAB03056.1" /db_xref="GI:1572495" /translaton="MAIPASTPPTPALVADPVGKLRQKGYCGAGGEGPADPLHQ AMAADDEFETFRFRPESDLAQLHTPGSAQORFQVSDLEFGGPNMGRILVAFVFA GALCAESVYKEKEPIVGVQYQDMVMVYLERLADMTIHSSGMAEFYLYDGLAEAR LRKSGMWSVRYLTGALVALGALVTGAFPAASK"</p>

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LOCUS	Mus musculus Bcl-1 (Bcl-1) mRNA, complete cds.		
DEFINITION	AF030769		
ACCESSION	AF030769.1	GI:2623249	
VERSION			
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 3476)		
AUTHORS	Rose, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and Macgregor, G.R.		
TITLE	Bcl-1 is required for testis homeostasis		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3476)		
AUTHORS	Rose, A.J. and Macgregor, G.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA		
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ORIGIN

Query Match 87.5%; Score 510; DB 10; Length 3473;
Best Local Similarity 92.3%; Pred. No. 5.9e-105;
Matches 537; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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DB 182 ATGGCGACCCGAGCTTGCGCCGACACACACGCGGCTCTGCTGAGCAGACTTGTAGTTAT 241
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DB 242 CAGCTGAGCGAAGAGGTTATGTCTGTGAGCTGCGCCCGGAGAGGCCACAGCGCGAC 301
QY 121 CGCGTGACCAAGCAATGGCGGAGCTGAGAGATGAGATGAGACCGGCTTCCGCGGAC 180
DB 302 CGCGTGACCAAGCAATGGCGGAGCTGAGAGATGAGATGAGACCGGCTTCCGCGGAC 361
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QY 241 CAGGCTCCGACGAACTTTTCAAGGCGGCGCCCACTGCGGCGCGCTTGTAGCTTTCTT 300
DB 422 CAGGCTCCGACGAACTTTTCAAGGCGGCGCCCACTGCGGCGCGCTTGTAGCTTTCTT 481
QY 301 CTCTTTGGGGCTGACCTGTGTCTGAGAGTGTCAACAAGAGATGAGAACCACTGTGTGGA 360
DB 482 GTCTTTGGGGCTGACCTGTGTCTGAGAGTGTCAACAAGAGATGAGAACCACTGTGTGGA 541
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DB 542 CAAGTGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATAAGGAGAGCGGCGCTTGAAGAGAGCGGCGG 480
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QY 481 CGTCTGGGGAGGGGAACTGGGCACTGATGAGAGCAAGTGTGACGCGGCGCGCTGTGCACTG 540
DB 662 CGTCTGGGGAGGGGAACTGGGCACTGATGAGAGCAAGTGTGACGCGGCGCGCTGTGCACTG 721
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DB 722 GGGGCGCTGTGTAAGTGTGAGGGGCTTTTGTGCTAGCAAGTGA 763

RESULT 14
LOCUS AX022531 581 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 8 from Patent BP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE unclassified.
1 Adams,J.M., Holmgren,S.P., Cory,S. and Gibson,L.M.
AUTHORS
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
JOURNAL apoptosis-controlling genes
PATENT: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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RLREGNMA"

ORIGIN

Query Match 85.9%; Score 501; DB 6; Length 581;
Best Local Similarity 91.4%; Pred. No. 7.9e-103;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGAGCTTGCGCCGACACACACGCGGCTCTGCTGAGCAGACTTGTAGTTAT 60
DB 1 ATGGCGACCCGAGCTTGCGCCGACACACACGCGGCTCTGCTGAGCAGACTTGTAGTTAT 60
QY 61 AAGCTGAGCGAAGAGGTTATGTCTGTGAGCTGCGCCCGGAGAGGCCACAGACTGAC 120
DB 61 AAGCTGAGCGAAGAGGTTATGTCTGTGAGCTGCGCCCGGAGAGGCCACAGCGCGAC 120
QY 121 CGCGTGACCAAGCAATGGCGGAGCTGAGAGATGAGATGAGACCGGCTTCCGCGGAC 180
DB 121 CGCGTGACCAAGCAATGGCGGAGCTGAGAGATGAGATGAGACCGGCTTCCGCGGAC 180
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DB 241 CAGGCTCCGACGAACTTTTCAAGGCGGCGCCCACTGCGGCGCGCTTGTAGCTTTCTT 300
QY 301 CTCTTTGGGGCTGACCTGTGTCTGAGAGTGTCAACAAGAGATGAGAACCACTGTGTGGA 360
DB 301 CTCTTTGGGGCTGACCTGTGTCTGAGAGTGTCAACAAGAGATGAGAACCACTGTGTGGA 360
QY 361 CAAGTGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CAAGTGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATAAGGAGAGCGGCGCTTGAAGAGAGCGGCGG 480
DB 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATAAGGAGAGCGGCGCTTGAAGAGAGCGGCGG 480
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DB 481 CGTCTGGGGAGGGGAACTGGGCACTGATGAGAGCAAGTGTGACGCGGCGCGCTGTGCACTG 540
QY 541 GGGGCGCTGTGTAAGTGTGAGGGGCTTTTGTGCTAGCAAGTGA 581
DB 541 GGGGCGCTGTGTAAGTGTGAGGGGCTTTTGTGCTAGCAAGTGA 581

RESULT 15
LOCUS AX030819 581 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 8 from Patent WO9735971.
ACCESSION AX030819
VERSION AX030819.1 GI:10046127
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

unidentified
unidentified
unclassified.

1
Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKER (AU) ; HOLMGREN SHAUN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)

FEATURES

location/Qualifiers

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RLREGNMA"

ORIGIN

Query Match 85.9%; Score 501; DB 6; Length 581;
Best Local Similarity 91.4%; Pred. No. 7.9e-103;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGGGACCCCAAGCTCGGCCCCCAGACACACGAGCTCTGTGCGACACTTTGTAGATTAT 60
DB 1 ATGCCGACCCCAAGCTCTCAACCCAGACACACGAGCTCTGTAGGCTGACTTTGTAGGCTAT 60
QY 61 AAGCTGAGGACAGAGGGTTATGCTGTGAGAGCTGGCCCCGGGAGAGGCCCAAGACTGAC 120
DB 61 AAGCTGAGGACAGAGGGTTATGCTGTGAGAGCTGGCCCCGGGAGAGGCCCAAGACTGAC 120
QY 121 CCGCTGCACCAAGCCATGCGGCGCTGTGAGAGCGAGTTGAGACCCGTTCCGCGCAC 180
DB 121 CCGCTGCACCAAGCCATGCGGCGCTGTGAGAGCGAGTTGAGACCCGTTCCGCGCAC 180
QY 181 TTCTCTGATCTGCGGCTCAGCTGATGACCCAGGCTCAGCCAGCAAGCTTCAAC 240
DB 181 TTCTCTGATCTGCGGCTCAGCTGATGACCCAGGCTCAGCCAGCAAGCTTCAAC 240
QY 241 CAGTCTCCGACGAATTTTCAAGGGGGCCCCAATGAGGGCCGCTTGTAGCCTTTCTT 300
DB 241 CAGTCTCCGACGAATTTTCAAGGGGGCCCCAATGAGGGCCGCTTGTAGCCTTTCTT 300
QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAAACAAGAGATGAACCACTGTGGGA 360
DB 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAAACAAGAGATGAACCACTGTGGGA 360
QY 361 CAAAGTCAGAGATGATGATGCTTACCTGAGAGCGCGGCTGTGACTGTGATCCACAGC 420
DB 361 CAAAGTCAGAGATGATGATGCTTACCTGAGAGCGCGGCTGTGACTGTGATCCACAGC 420
QY 421 AATGGGGGCTGGGCGGAGTTCAAGCTCTATACGGGGAAGGGCCCTGAGAGAGCGCGG 480
DB 421 AATGGGGGCTGGGCGGAGTTCAAGCTCTATACGGGGAAGGGCCCTGAGAGAGCGCGG 480
QY 481 CGTCTGCGGAGAGGGAAGTGGGCATCATGAGGACAGTGTGACGAGGGGCGGTGCACTG 540
DB 481 CGTCTGCGGAGAGGGAAGTGGGCATCATGAGGACAGTGTGACGAGGGGCGGTGCACTG 540
QY 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTAGCAAGTG 581
DB 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTAGCAAGTG 581

Search completed: March 29, 2004, 06:11:55
Job time : 2776.74 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:18:04 ; Search time 2274.9 seconds
(without alignments)

7652.923 Million cell updates/sec

Title: US-09-155-327G-6

Perfect score: 583

Sequence: 1 atgcgcacccacccagctcgcg.....cttttctgtaagtaagaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_prg:*
27: em_gss_vrl:*
28: gb_gsal:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572.4	98.2	582	29	AY421020 Homo sapi
2	550	94.3	804	9	AL157542 DKFZP761D
3	548.4	94.1	1030	10	BE793530 601590016
4	522.8	89.7	582	29	AY421022 Mus muscu

5	522.8	89.7	1949	11	AK015644 Mus muscu
6	522.8	89.7	3487	11	AK004680 Mus muscu
7	521.2	89.4	969	12	BY715200 BY715200
8	483.4	82.9	697	12	BT770566 BT770566
9	465.6	79.9	967	13	BUS03850 BUS03850
10	443	76.0	626	14	CA391923 CA391923
11	417.6	71.6	643	12	BI910270 BI910270
12	397	68.1	815	10	BF785366 BF785366
13	381.8	65.5	623	14	CB578463 CB578463
14	375.4	64.4	854	11	AK013244 AK013244
15	364.2	62.5	792	12	BG298789 BG298789
16	360	61.7	548	14	CA407839 CA407839
17	359	61.6	869	13	BUS57268 BUS57268
18	359	61.6	872	13	BUS57410 BUS57410
19	357.2	61.3	540	10	AM258810 AM258810
20	332	56.9	437	14	CB790932 CB790932
21	331.2	56.8	440	14	CB749817 CB749817
22	326.8	56.1	758	12	BI764428 BI764428
23	317.8	54.5	1053	13	BU931540 BU931540
24	311.2	53.4	327	29	AY421021 Pan trogl
25	305.2	52.3	559	13	CF533813 CF533813
26	297.8	51.1	749	12	BG677345 BG677345
27	294.2	50.5	645	13	BY740551 BY740551
28	293.8	50.4	645	13	BF204905 BF204905
29	290	49.7	601	10	CB804140 CB804140
30	289.2	49.6	410	9	AA596919 AA596919
31	288	49.4	362	14	BQ646339 BQ646339
32	282.6	48.5	1064	13	BY285647 BY285647
33	268	46.0	460	13	BY253191 BY253191
34	264.4	45.4	449	13	BY253191 BY253191
35	257.6	44.2	433	10	AM326901 AM326901
36	257.4	44.2	430	14	CB760687 CB760687
37	240	41.2	457	10	BB856021 BB856021
38	239.8	41.1	853	14	CA964774 CA964774
39	237.4	40.7	353	13	BY312773 BY312773
40	236.6	40.6	731	14	CF282823 CF282823
41	235.6	40.4	756	14	CF374729 CF374729
42	233.2	40.0	425	13	BY251598 BY251598
43	230.6	39.6	467	13	BY253189 BY253189
44	229.2	39.3	452	14	CB766193 CB766193
45	226.4	38.8	302	13	BY356166 BY356166

ALIGNMENTS

RESULT 1
LOCUS AY421020
DEFINITION Homo sapiens BC1212 gene, VIRUAL TRANSCRIPT, partial sequence.
ACCESSION AY421020
VERSION AY421020.1 GI:39776977
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,D.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,D.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

Source

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/mol_type="genomic DNA"
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ORIGIN

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Best Local Similarity 99.0%; Pred. No. 1.5e-120;
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 ATGGGACCCGAGCTTGGGCGCCAGACACAGCGGCTCTGTGGCAGACTTTGTAGGTTAT 60
1 ATGGGACCCGAGCTTGGGCGCCAGACACAGCGGCTCTGTGGCAGACTTTGTAGGTTAT 60
61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGCCCAAGACTGAC 120
61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGCCCAAGACTGAC 120
121 CCGGTGACCAAGCAATCGGGGAGCTGAGATGATGAGTCCGCGCTCCGGCGCACC 180
121 CCGGTGACCAAGCAATCGGGGAGCTGAGATGATGAGTCCGCGCTCCGGCGCACC 180
181 TTCTCTGATCTGGGCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 240
181 TTCTCTGATCTGGGCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 240
241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTTTGAGCTTTCTT 300
241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTTTGAGCTTTCTT 300
301 CTCTTTGGGGCTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
301 CTCTTTGGGGCTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
361 CAATGACAGAGT 420
361 CAATGACAGAGT 420
421 AGTGGGGCTGGGCGGAGTTCAAGCTCTATACCGGGGACCGGGCCCTGAGAGAGCGCG 480
421 AGTGGGGCTGGGCGGAGTTCAAGCTCTATACCGGGGACCGGGCCCTGAGAGAGCGCG 480
481 CGTCTGCGGAGGAGAACTGGGCACTCAAGTGAAGCAAGTGTGACGGGGCCGTGGCACTG 540
481 CGTCTGCGGAGGAGAACTGGGCACTCAAGTGAAGCAAGTGTGACGGGGCCGTGGCACTG 540
541 GGGGCGCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 582
541 GGGGCGCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 582

RESULT 2

AL157542

LOCUS

DEFINITION DKFZ761D0816.r1 761 (synonym: hamy2) Homo sapiens cDNA clone

AL157542

ACCESSION AL157542.1 GI:7057943

VERSION

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eubacteria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 804)

Ansoerge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.

TITLE EST (Ansoerge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.)

JOURNAL

Unpublished (1999)

Contact: MIPS

MIPS

Ingo Isenhardt Landstr.1, D-65764 Neuberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;

Sequenced by EMBL (European Molecular Biology Laboratories,

Heidelberg/Germany) within the cDNA sequencing consortium of the

German Genome Project.

No sequence available.

This clone (DKFZ761D0816) is available at the RZPD in Berlin.

Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1..804
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ761D0816"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="761 (synonym: hamy2)"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 94.3%; Score 550; DB 9; Length 804;
Best Local Similarity 96.6%; Pred. No. 2.3e-115;
Matches 575; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

1 ATGGGACCCGAGCTTGGGCGCCAGACACAGCGGCTCTGTGGCAGACTTTGTAGGTTAT 60
124 ATGGGACCCGAGCTTGGGCGCCAGACACAGCGGCTCTGTGGCAGACTTTGTAGGTTAT 193
61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGCCCAAGACTGAC 120
194 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGGCCCGGGAGAGGCCCAAGACTGAC 253
121 CCGGTGACCAAGCAATCGGGGAGCTGAGATGATGAGTCCGCGCTCCGGCGCACC 180
254 CCGGTGACCAAGCAATCGGGGAGCTGAGATGATGAGTCCGCGCTCCGGCGCACC 313
181 TTCTCTGATCTGGGCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 240
314 TTCTCTGATCTGGGCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGAT 373
241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTTTGAGCTTTCTT 300
374 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCGGCTTTGAGCTTTCTT 433
301 CTCTTTGGGGCTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
434 GTCTTTGGGGCTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 493
361 CAATGACAGAGT 420
494 CAATGACAGAGT 553
421 AGTGGGGCTGGGCGGAGTTCAAGCTCTATACCGGGGACCGGGCCCTGAGAGAGCGCG 480
554 AGTGGGGCTGGGCGGAGTTCAAGCTCTATACCGGGGACCGGGCCCTGAGAGAGCGCG 612
481 CGTCTGCGGAGGAGAACTGGGCACTCAAGTGAAGCAAGTGTGACGGGGCCGTGGCACTG 540
613 CGTCTGCGGAGGAGAACTGGGCACTCAAGTGAAGCAAGTGTGACGGGGCCGTGGCACT- 671
541 GGGGCGCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 583
672 GGGGCGCTGTAACTGTAGGGGCTTTTGTCTAGCAAGTGA 714

RESULT 3
LOCUS BE793530
DEFINITION BE793530 1030 bp mRNA linear EST 20-SEP-2000
601590016r1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
rRNA sequence.
ACCESSION BE793530
VERSION BE793530.1 GI:10214832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eumetazoa; Eutheria; Chordates; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1030)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
 Plate: L1CM600 row: p column: 04
 High quality sequence start: 5
 High quality sequence stop: 709.

FEATURES	Location/Qualifiers
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source
1. .1030
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/db_xref="taxon:9606"
/clone="IMAGE:3944307"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NH_MGC_7"
/note="Organ: lung; Vector: pOTB1; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
insert: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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ORIGIN

Query Match	94.1%;	Score	548.4;	DB	10;	Length	1030;
Best Local Similarity	96.4%;	Pred.	NO. 6e-115;				
Matches	561;	Conservative	0;	Mismatches	21;	Indels	0;
						Gaps	0;

QY	ATGGCAGACCCAGGCTGGGCCCCAGACACAAGGGCTCTGGTGGAGAACTTTGTAGGTTAT	60
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QY	AAAGCTGAGGAGAAAGGTTATGTCTGTGGAGCTGGCCCCGGAGAGGAGGCTCAGACAGCTTAC	120
Db	AAAGCTGAGGAGAAAGGTTATGTCTGTGGAGCTGGCCCCGGAGAGGAGGCTCAGACAGCTTAC	263
QY	CCGGTGAACCAAGCAGATGGGGGAGGTGGAGATGAGTTGAGACCCGGCTTCGGAGCAGACC	180
Db	CCAGTGAACCAAGCAGATGGGGGAGGTGGAGATGAGTTGAGACCCGGCTTCGGAGCAGACC	323
QY	TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGAGCTCAGGCCAGACAAAGCTTAC	240
Db	TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGAGCTCAGGCCAGACAAAGCTTAC	383
QY	CAGGTCGCCACGAACTTTCAAGGGGGGCCCAACTGGGAGCGGCTGTGAGCCTTTCTT	300
Db	CAGGTCGCCACGAACTTTCAAGGGGGGCCCAACTGGGAGCGGCTGTGAGCCTTTCTT	443
QY	CTCTTTGGGGGTGACGTGTGGCTGAGAGTGAACAAGAGATGAAACAATCTGTGGGA	360

Db	444	GTCCTTTGGGCGTCACTGTGTGCTGAGAGTGCACAAAGAGAGATGGAAACCACTGGTGGGA	5030
Qy	361	CAAGTGAAGAAGTGAATGGTGGGCTAACCTGGAGAAGGGGGCTGATCGACTGGATTCACAGC	4200
Db	504	CAAGTGAAGAAGTGAATGGTGGGCTTAACCTGGAGAAGGGGGCTGATCGACTGGATTCACAGC	5630
Qy	421	AGTGGGGGCTGGGCGAGATTCAACAGCTCTATACGGGGACGGGGGCTCTGAGAGAGCGCGG	4800
Db	564	AGTGGGGGCTGGGCGAGATTCAACAGCTCTATACGGGGACGGGGGCTCTGAGAGAGCGCGG	6230
Qy	481	CGTCTGGGGAAGGGGAATCGGGCAATGATGAGAGACAGTCTGACGGGGGCCGTGGCACTG	5400
Db	624	CGTCTGGGGAAGGGGAATCGGGCAATGATGAGAGACAGTCTGACGGGGGCCGTGGCACTG	6830
Qy	541	GGGGCCCTGGTAACCTGATAGGGGCGTTTTTGTCTACCAAGTGA	582
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RESULT 4	AY421022	582 bp	DNA	linear	GSS 17-DEC-2001
LOCUS	AY421022				
DEFINITION	Mus musculus Bcr2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY421022				
VERSION	AY421022.1	GI:39776979			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				

ORGANISM

REFERENCE	1 (bases 1 to 582)
AUTHORS	Clark, A.G., Glandowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 582)
 AUTHORS Clark, A.G., Glatowski, S., Nielson, R., Thomas, P., Kejarivala, A.,

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) *Celera Genomics*, 45 West Gude Drive,

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES

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gene

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ORIGIN

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Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0

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Db 1 ATGGCGACCCCAAGCTCTCAACCCACAGACACGGGCTCTGTGGCTAATTTGAAGGCTAT 60

Qy 61 AAGCTGAGGCAACAAAGGTTATGTCTGTGGAGCTGGCCCGGGGAGGGGCCAGAGTGAC 120

Db 61 AAGCTGAGGCAACAAAGGTTATGTCTGTGGAGCTGGGCCCTGGGGGAAAGGCCCAAGCCGCGAC 120

Qy 121 CGGCTGACCAACAGCCATGGGGGAGTGGAGATGAAGTTGAGACCGGCTTCCGGCGACCC 180

Query Match 89.7%; Score 522.8; DB 11; Length 1949;
 Best Local Similarity 93.6%; Pired.No.5.8e-109;
 Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGTGCCCCGGGAGGGCCACAGCTGAC 120
DB 192 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGTGCCCCGGGAGGGCCACAGCTGAC 251
QY 121 CCGCTGACACCAACCATGCGGGCAGCTGAGATGAGTGTGAGACCCGCTTCGGCGCAC 180
DB 252 CCGCTGACACCAACCATGCGGGCAGCTGAGATGAGTGTGAGACCCGCTTCGGCGCAC 311
QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCCAAGCTCAGCCAGAGAGCTTAC 240
DB 312 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCCAAGCTCAGCCAGAGAGCTTAC 371
QY 241 CAGGCTCCGAGCACTTTTTCAGGGGGGCCCACTGGGGCGGCTGTAGGCTTCTT 300
DB 372 CAGGCTTCCGAGCACTTTTTCAGGGGGGCCCTTAACTGGGGCGGCTGTAGGCTTCTT 431
QY 301 CTCTTTGGGGCTGCTGCTGTGAGAGTGTCAAGAGAGAGTGTGAACTCAGTGTGGA 360
DB 432 GTCTTTGGGGCTGCTGCTGTGAGAGTGTCAAGAGAGAGTGTGAACTCAGTGTGGA 491
QY 361 CAAAGTGAGAGAGTGTGAGTGTGAGCTTCTGAGAGACCGGGCTGTGACTGTGATCCACAGC 420
DB 492 CAAAGTGAGAGAGTGTGAGTGTGAGCTTCTGAGAGACCGGGCTGTGACTGTGATCCACAGC 551
QY 421 AATGGGGGGCTGGGGCGGAGTTCACAGCTCTTATAGGGGAGCGGGGCTTGGAGAGGGCGGG 480
DB 552 AATGGGGGGCTGGGGCGGAGTTCACAGCTCTTATAGGGGAGCGGGGCTTGGAGAGGGCGGG 611
QY 481 CGTCTGGGGAGGGGAACTGGGATCATGTGAGAGAGAGTGTGAGCGGGCGGAGGACAGT 540
DB 612 CGTCTGGGGAGGGGAACTGGGATCATGTGAGAGAGAGTGTGAGCGGGCGGAGGACAGT 671
QY 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTTCAGCAAGTGA 582
DB 672 GGGGCGCTGTAACTGTAGGGGCTTTTGTTCAGCAAGTGA 713

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RESULT 6
 AK004680
 LOCUS
 DEFINITION
 AK004680 3487 bp. mRNA. linear. HTC 20-SHP-2003
 library, clone:1200009L24 Product:Bcl2-like 2, full insert
 sequence.
 ACCESSION
 AK004680
 VERSION
 AK004680.1 GI:12936027
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 TITLE
 High-efficiency full-length cDNA cloning
 JOURNAL
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE
 99279253
 PUBMED
 10349636

REFERENCE
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Komu, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE
 Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE
 20499374
 PUBMED
 11042159

REFERENCE
 3

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
 Komu, H., Akiyama, J., Nishii, K., Kiteunai, T., Tashiro, H., Itoh, M.,
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsunoto, H., Sakaiguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Iizawa, M., Oikari, E., Wataiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 11076861

TITLE

The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3487)

TITLE

JOURNAL

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
 Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
 Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
 Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Iizawa, M.,
 Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komu, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsumura, T., Miyazaki, A., Nishii, K.,
 Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
 Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D.,
 Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagami, W., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE

JOURNAL

REFERENCE

AUTHORS

COMMENT

Submitted (10-JUL-2000) Yoshihide Hayashizaki: The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
 further details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in RIKEN
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5' GAGAGGAGAGCGGGCGCGACGAGTGTGTTTGTGTTTGTGTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. Second
 strand cDNA was prepared with the primer adapter of sequence [5'
 GAGAGGAGAGGATCAAGAGCTCAATTAATTAATTAACCCGCCCC 3']. cDNA was
 cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
 XhoI. Host: SOLR.

FEATURES
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209 ATGGGACCCCAAGCTCTGGGCCCCGAGACACCGGCTCTGTGGGAGAGCTTTGAGGTTAT 268
61 AAGCTGAGGACGAGAGGTTATGTCTGTGAGAGCTGGCCCCGAGAGGCCCCGAGAGCTGAC 120
269 AAGCTGAGGACGAGAGGTTATGTCTGTGAGAGCTGGCCCCGAGAGGCCCCGAGAGCTGAC 328
121 CCGCTGACCAAGGCTATGGGCGACAGTGGAGATGATGTCGAGAGCCGCTTCCGCGCAGC 180
329 CCGCTGACCAAGGCTATGGGCGACAGTGGAGATGATGTCGAGAGCCGCTTCCGCGCAGC 388
181 TTCTCTGATCTGGGCGCTCAGCTGATGTGACCCCAAGCTCTGAGCCGACGAGCTTTAC 240
389 TTCTCTGATCTGGGCGCTCAGCTGATGTGACCCCAAGCTCTGAGCCGACGAGCTTTAC 448
241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCCCAACTGGGGCGCTTGTAGCTTTCTTT 300
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301 CTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAGAGATGGAACCACTGGTGGGA 360
509 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAGAGATGGAACCACTGGTGGGA 568
361 CAACTGACGAGAGTGTGTGTGTGAGAGTGTGTGAGAGCGGCTGTGTGAGTGTGATCAAC 420
569 CAACTGACGAGAGTGTGTGTGTGAGAGTGTGTGAGAGCGGCTGTGTGAGTGTGATCAAC 628
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481 GCTTGGCGGAGGAGGAGCTGGGCGATCACTGAGAGACAGTGTGAGCGGGCGCTGGGCGATG 540
689 GCTTGGCGGAGGAGGAGCTGGGCGATCACTGAGAGACAGTGTGAGCGGGCGCTGGGCGATG 748
541 GGGGCGCTGTACTGTGAGGGGCTTTTGTGTAGCAAGTGA 582
749 GGGGCGCTGTACTGTGAGGGGCTTTTGTGTAGCAAGTGA 790

RESULT 7
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LOCUS BY715200 RIKEN full-length enriched, adult male testis Mus musculus
DEFINITION CDNA clone 4930488D08 5', mRNA sequence.
ACCESSION BY715200
VERSION BY715200.1 GI:27128317
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 969)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oseto, N., Saito, R., Suzuki, H., Yamanka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanpin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Brack, D., Bruscia, V. A.,
Chochois, C., Corbani, L. E., Coumans, S., Daille, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Glessi, C., Godzik, A., Gough, J., Grimmond, S.,
Guernincich, S., Hirokawa, N., Jackson, J. D., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Matsuda, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semp, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, T.,
Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yangisawa, M., Yang, T.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Haseizume, N., Imocani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

JOURNAL
MEDLINE
PUBMED
22354683

COMMENT

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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashizaki, K., Hirozane, T., Hori, F.,
Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, N.,
Nomura, K., Nunakazu, R., Ohno, M., Oseto, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 675-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Science Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES

source

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 QY 478 CGGCTGTGGGAGAGGGGAACTGGGCA-TCAGTGAAGACAG-TGCTGACGGGGGCGGTG 535
 DB 625 CGGGTGTGGGAGAGGGGAACTGGGCACTCAGTGAAGACAGTTGCTGACGGGAGCCGTGG 684
 QY 536 CACTGGGGGCGCT 548
 DB 685 CACTGGGGGCGCT 697
 RESULT 9
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 LOCUS AGENCOURT_10030867 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491566
 DEFINITION 5', mRNA sequence.
 ACCESSION BUS03850
 VERSION BUS03850.1 GI:22810083
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 967)
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsbbs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
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 High quality sequence stop: 524.
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 Average insert size 3.3 kb. Library enriched for
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 Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 79.9%; Score 465.6; DB 13; Length 967;
 Best Local Similarity 92.5%; Pred. No. 5,4e-96;
 Matches 544; Conservative 0; Mismatches 39; Indels 5; Gaps 5;

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 QY 301 CTTTGGGGGCTGACAGTGTGCTGAGAGTGTCAACAAGAGATGATAACCACTGGTGGGA 360
 DB 430 GTCTTTGGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAGAGATGATAACCACTGGTGGGA 489
 QY 361 CAAGTGCAGAGATGGATGTGTGACCTTA-CTTGAAGACGCGGTGTGCACTGATTCACAG 419
 DB 490 CAGTGCAGAGATGGATGTGTGACCTTAAGAGACACAGTGTGCTGATGATTCACAG 549
 QY 420 CAGT-GGGGGCTGGCGGAGTTCAACAGCTTATACGGGGAC-GGGGCCCTTGAGAGAGCG 477
 DB 550 CAGTGGGGGCTGGCGGAGTTCAACAGCTTATACGGGGACGGGGGCCCTTGAGAGAGCA 609
 QY 478 CGGCTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGAC-GGGGGCGGTGGC 536
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 DB 670 ACTGGGGGCGCTGGTAACTGTAAAGGGGCTTTTGTAGCAAGTGAA 717
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 LOCUS cs20c09.y1 Human Retinal pigment epithelium/choroid cDNA cs20c09
 DEFINITION (un-normalized, unambiguated): cs Homo sapiens cDNA clone
 5', mRNA sequence.
 ACCESSION CA391923
 VERSION CA391923.1 GI:24724221
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 626)
 Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
 Expressed sequence tag analysis of human RPE/choroid for the
 NEBank Project: Over 600 non-redundant transcripts, novel genes
 and splice variants
 Mol. Vis. 8 (4), 205-220 (2002)
 JOURNAL MEDLINE 22103460
 PUBMED 12107410
 COMMENT Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 20 row: C column: 09
 Seq primer: M13R1 reverse primer (ABI).
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 eyes (75-80 years old) yielded approximately 600 mg of

dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp).

<http://www.invitrogen.com/>. The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/Mui sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 76.0%; Score 443; DB 14; Length 626;
Best Local Similarity 98.7%; Pred. No. 6,6e-91;
Matches 446; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGAGCTTGGCCCGACACACAGGGCTCTGTGGCAGACTTTGTAGTTAT 60
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QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCCAAGCTGAC 120
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QY 121 CCGCTGACCAAGCCATGCGGGGAGGATGATGTGAGACCCGCTTCCGGCGCAGC 180
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QY 301 CTCTTTGGGGCTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
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QY 361 CAGGTGAGAGAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
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RESULT 11
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LOCUS 60306943F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',
DEFINITION mRNA sequence.
ACCESSION BI910270 GI:16173653
VERSION BI910270.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 643)
NIH-MGC http://mgs.nci.nih.gov/
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11548 row: j column: 23
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ORIGIN

Query Match 71.6%; Score 417.6; DB 12; Length 643;
Best Local Similarity 93.7%; Pred. No. 4,4e-85;
Matches 446; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 1 ATGGCGACCCGAGCTTGGCCCGACACACAGGGCTCTGTGGCAGACTTTGTAGTTAT 60
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QY 181 TTCTGTATCTGGCGGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 240
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DB 440 GTCTTTGGGGCTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 499
QY 360 ACAAGTGAAGAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 419
DB 500 ACAAGTGAAGAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 559
QY 420 CAGTGGGGGCTGGCGGAGTTCAAGCTCTATAAGGGGAGCGGGCCCTGAGAGAG 475
DB 560 CAGTGGGGGCTGGCGGAGTTCAAGCTCTATAAGGGGAGCGGGCCCTGAGAGAG 615

RESULT 12
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LOCUS 602111728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
DEFINITION 5', mRNA sequence.
ACCESSION BF785386 GI:12090422
VERSION BF785386.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 815)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL

COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LHM9853 row: h column: 07
 High quality sequence start: 3
 High quality sequence stop: 650.
 Location/Qualifiers

FEATURES

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ORIGIN

Query Match 68.1%; Score 397; DB 10; Length 815;
 Best Local Similarity 91.1%; Pred. No. 2.6e-80;
 Matches 500; Conservative 0; Mismatches 40; Indels 9; Gaps 7;

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 141 GGCAGCTGAGAGTGAAGTTGAGACCCGCTTCCGGGCGACCTTCTCTGATCTGGGGGTCA 200
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 201 GCTGATGTGACCCAGGCTCAGCCAGCAAGCTTCAACCAGGTTCCGACGAATTTT 260
 180 GCTACACGTCACCGGCTCAGCCAGCAAGCTTCAACCAGGTTCCGACGAATTTT 239
 261 TCAGAGGGGGCCCCAAGCTGGGGCCGCTTGTAGCCCTTCTTCTTTGGGGGTGCACTGTG 320
 240 CCAAGGGGGCCCTAAGCTGGGGCCGCTTGTAGCCCTTCTTCTTTGGGGGTGCACTGTG 296
 321 TGTCTGAGAGTGTCAACAGAGATGGAACCACTGTTGGGACAGAGTGCAGAGTGGATGCT 380
 297 TGTCTGAGAGTGTCAACAGAGATGGAACCACTGTTGGGACAGAGTGCAGAGTGGATGCT 355
 381 GGCCTTACCTGAGAGAGCGCGCTGTGACTGATTCACAGCAGTGGGGGTGAGGAGTT 440
 356 GGCCTTACCTGAGAGAGCGCGCTGTGACTGATTCACAGCAGTGGGGGTGAGGAGTT 415
 441 CACAGCTTATACGGGGAACGGGGCCCTGAGAGAGGCGGCGCTTCCGAGAGGGAATG 500
 416 CACAGCTTATACGGGGAACGGGGCCCTGAGAGAGGCGGCGCTTCCGAGAGGGAATG 473
 501 GGCATCAGTGAAGACAGTGTCTGACGGGGCCCTGAGCACTGGGGGCTTGTGTAATCTGTGG 560
 474 GGCATCAGTGAAGACAGTGTCTGACGGGGCCCTGAGCACTGGGGGCTTGTGTAATCTGTGG 532
 561 GGCCTTTT 569

Db 533 GGCCTTTT 541

RESULT 13
 CB578463
 LOCUS
 DEFINITION AMGN:NCI-RNDG1-00100-H10-A nrdg1 (10855) Rattus norvegicus cDNA
 accession CB578463
 version CB578463.1 GI:29522504
 keywords EST.
 source Rattus norvegicus (Norway rat)
 organism Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 623)
 AUTHORS Amgen EST Program
 TITLE Amgen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick
 Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00100 row: h column: 10.
 Location/Qualifiers

FEATURES

source

1..623
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="nrdg1-00100-H10"
 /tissue_type="Dorsal Root Ganglia"
 /clone_lib="nrdg1 (10855)"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; rat dorsal root ganglia"

ORIGIN

Query Match 65.5%; Score 381.8; DB 14; Length 623;
 Best Local Similarity 92.6%; Pred. No. 6.9e-77;
 Matches 401; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

1 ATGGCACCCTCAGCTGGCCCCAGACACACAGGCGCTGTGTGAGCACTTTGTAGGTTAT 60
 191 ATGGCACCCTCAGCTGTATATCTGTGAGCTGGCCCTGAGGAGAGGCCACAGCCAGC 250
 61 AAGCTGAGGACAAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGAGGCCACAGCTGAC 120
 251 AAGCTGAGGACAAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGAGGCCACAGCTGAC 310
 121 CCGCTCACCAAGCCATGCGGGCAGCTGAGATGATTTGAGACCCGCTTCCGGGCGACC 180
 311 CCGCTCACCAAGCCATGCGGGCAGCTGAGATGATTTGAGACCCGCTTCCGGGCGACC 370
 181 TTCTCTGATCTGCGGCTCAGCTGATGATGACCCCAAGCTCAGCCCAAGGCTTCCACC 240
 371 TTCTCTGATCTGCGGCTCAGCTGATGATGACCCCAAGCTCAGCCCAAGGCTTCCACC 430
 241 CAGGCTCCGACGAATTTTTCAGAGGGGGCCCCCACTGGGGCGGCTTGTAGCTTTCTT 300
 431 CAGGTTCCGACGAATTTTTCAGAGGGGGCCCCCACTGGGGCGGCTTGTAGCTTTCTT 490
 301 CTCTTTGGGGCTGCACTGTGTGTGAGATGTCAACAAGAGATGGAACCACTGTGTGGA 360
 491 GTCTTTGGGGCTGCACTGTGTGTGAGATGTCAACAAGAGATGGAACCACTGTGTGGA 550
 361 CAAATGCAAGAGTGTGTGTGTGCTTACCTGAGACCGGCGCTGTGATCCAGAC 420
 551 CAAATGCAAGAGTGTGTGTGTGCTTACCTGAGACCGGCGCTGTGATCCAGAC 610
 421 AGTGGGGGCTGGG 433
 611 AGTGGGGGCTGGG 623

RESULT 14	AK013244	554 bp	mRNA	linear	HTC 20-SEP-2003
LOCUS	AK013244				
DEFINITION	Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810455A13 product:Bc12-like 2, full insert sequence.				
ACCESSION	AK013244				
VERSION	AK013244.1	GI:12650487			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
REFERENCE	Carninci, P. and Hayashizaki, Y.				
AUTHORS	1				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasahagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 394 multichannel sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
MEDLINE					
PUBMED					
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
MEDLINE	6 (bases 1 to 854)				
PUBMED					
REFERENCE	6				
AUTHORS	Arakawa, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arai, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaitakawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takaheishi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamamatsu, M. and Hayashizaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suhei-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail:genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ , Tel:81-45-503-9222, Fax:81-45-503-9216]				

COMMENT
Please visit our web site (<http://genome.ssc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAAGAGGATCCCAAGACCTTTTCTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalisation to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCTCGAGTTAATAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SctI. Cloning sites, 5' end: XhoI, 3' end: SctI. Host: SOLR.

FEATURES
source
Location/Qualifiers
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 /db_xref="MGI:1902183"
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AMAAAGDEFFTRFRRTSLDAOLHTPGSAOGRFTGVNSDELFOGGNMGRLVAFFVF
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LHGICFLPMGMGAGRG"

CDS

ORIGIN
Query Match 64.4%; Score 375.4; DB 11; Length 854;
Best Local Similarity 91.7%; Pred. No. 2,3e-75;
Matches 397; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db

1 ATGGCGACCCCGAGCTTGCGGCCCGCACACACGCGGCTTCGTGGCGACTTTGATGTTAT 60
196 ATGGCGACCCCGAGCTCAACCCCGACACACGCGGCTTCGTGGCGACTTTGATGTTAT 255
61 AAGCTGAGCGAAGAGGTTATGTCTGTGGAGCTTGCCCCGGGGAGGGCCCGACAGCTGCAC 120
256 AAGCTGAGCGAAGAGGTTATGTCTGTGGAGCTTGCCCCGGGGAGGGCCCGACAGCTGCAC 315
121 CCGCTGACCAAGCATGCGGGGAGCGTGGAGTAGTTCAGAACCCGCTTCCGGCGACCC 180
Db 316 CCGCTGACCAAGCATGCGGGGAGCGTGGAGTAGTTCAGAACCCGCTTCCGGCGACCC 375
181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGACGCTCAGCCCGACAACGCTTCAAC 240
Db 376 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGACGCTCAGCCCGACAACGCTTCAAC 435
241 CAGGCTTCCGACGAATTTTCAAAGGGGGGCCCAACTGGGGCGGCTTTGATGCTTTT 300
Db 436 CAGGCTTCCGACGAATTTTCAAAGGGGGGCCCTTAATCGGGGCGGCTTTGATGCTTTT 495
301 CTCTTTGGGGGCTGACTGTGTGCTGAGAGTGTCACAAAGAGAGTGAACAACAGTGGTGGGA 360
Db 496 GTCTTTGGGGGCTGCTGTGTGCTGAGAGTGTCACAAAGAGAGTGAAGACCCTTTGTGGGA 555
361 CAAGTGCAGAGTAGTGTGAGCTTACTCTGGAGACGGGCTGTGATCGACTGATCCAGAC 420
Db 556 CAAGTGCAGAGTAGTGTGAGCTTACTCTGGAGACAGTGTGCTGATCGATCCAGAC 615

QY 421 AGTGGGGCTGGG 433
 DB 616 AGTGGGGCTGGG 628

RESULT 15

BG398789

LOCUS

602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215 5',
 mRNA sequence.

ACCESSION

BG398789

VERSION

BG398789.1 GI:13063794

KEYWORDS

EST, Mus musculus (house mouse)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

792 bp mRNA linear EST 21-FEB-2001
 NIH-MGC http://mgs.nci.nih.gov/
 1 (bases 1 to 792)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: rsraus@remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM10394 row: e column: 08
 High quality sequence stop: 713.

FEATURES

source

1..792
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:4511215"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_94"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 62.5%; Score 364.2; DB 12; Length 792;
 Best Local Similarity 91.1%; Pred. No. 8.2e-73;
 Matches 398; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

QY 1 ATGCGACCCCAAGCTCGGCCCCAGACACAGGGCTCTGTGGCAGACTTTGTAGTTAT 60
 DB 99 ATGCGACCCCAAGCTCGGCCCCAGACACAGGGCTCTGTAGTTGTAGTTAT 158
 QY 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGGTGGCCCCGGGAGAGGCCAGAGCTGAC 120
 DB 159 AAGCTGAGGAGAAAGGTTATGTCTGTGAGGTGGCCCCGGGAGAGGCCAGAGCTGAC 218
 QY 121 CCGCTGACCAAGCAGATGCGGAGCTGAGATGATTGAGACCCGCTTCGGGCGACC 180
 DB 219 CCGCTGACCAAGCAGATGCGGAGCTGAGATGATTGAGACCCGCTTCGGGCGACC 278
 QY 181 TTCTGTGATCTGGCGGCTCAGCTGATGTGACCCCAAGCTCAGCCAGCAAGCTTCACC 240
 DB 279 TTCTGTGATCTGGCGGCTCAGCTGATGTGACCCCAAGCTCAGCCAGCAAGCTTCACC 337
 QY 241 CAGGTTCTCGAAGAACTTTTCAAGGGGGCCCCCACTGGGGCCGCTGTAGCCTTTCTT 300
 DB 338 CAGGTTCTCGAAGAACTTTTCAAGGGGGCCCCCACTGGGGCCGCTGTAGCCTTTCTT 397
 QY 301 CTCTTGGGGCTGACGTGTGTCTGAGAGTGTCAACAAGAGATGAACCACTGGTGGGA 360

DB 398 GTCTTTGGGGCTGGCCCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGTGGGA 457
 QY 361 CAAGTGCAGAGATGAGATGAGTGGCTTACCTGGAGACGGGCTGTGCACTGATCAGAGC 420
 DB 458 CAAGTGCAGAGATGAGATGAGTGGCTTACCTGGAGACAGCTGTGCTGACTGATCAGAGC 517
 QY 421 AGTGGGGCTGGGCGGA 437
 DB 518 AGTGGGGCTGGTAAGA 534

Search completed: March 29, 2004, 07:28:08
 Job time : 2302.9 secs

immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 583; DB 2; Length 583;

Best Local Similarity 100.0%; Pred. No. 7,3e-136; Mismatches 0; Gaps 0; Matches 583; Conservative 0; Indels 0; Gaps 0;

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QY 1 ATGGGAGCCCGAGCTGGGCCCCGAGACACAGGGGCTCTGGTGGGAGACTTTGAGTTAT 60
DB 1 ATGGGAGCCCGAGCTGGGCCCCGAGACACAGGGGCTCTGGTGGGAGACTTTGAGTTAT 60
QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCGAGAGCTGAC 120
DB 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCGAGAGCTGAC 120
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DB 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATAGATTGAGACCCGCTTCCGGCGAC 180
QY 181 TTCTCTGATCTGGCGGCTCACTGATGATGACCCGAGCTCAGCCGAGCAAGCTTAC 240
DB 181 TTCTCTGATCTGGCGGCTCACTGATGATGACCCGAGCTCAGCCGAGCAAGCTTAC 240
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DB 241 CAGGTCTCCGACGAATTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
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QY 421 AGTGGGGGCTGGGGGAGGTTCACAGCTCTATACGGGGGAGCGGGCCCTGGAGAGCG 480
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QY 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGAAGCGGGGCGGTGG 540
DB 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGAAGCGGGGCGGTGG 540
QY 541 GGGGGCCCTGGTACTGTAAGGGGCTTTTGTGTAAGATGAA 583
DB 541 GGGGGCCCTGGTACTGTAAGGGGCTTTTGTGTAAGATGAA 583

```

RESULT 2
AA25134
ID AAX25134 standard; DNA; 583 BP.

AA25134;
05-JUL-1999 (first entry)
Human bcl-w gene derivative.
Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
animal model; ss.
Homo sapiens.
MO913710-A1.
25-MAR-1999.

16-SEP-1998; 98WO-AU000764.
16-SEP-1997; 97AU-00009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

Cory S, Adams J, Print C, Gibson L, Koentgen F;

WPI; 1999-243690/20.
P-PSDB; AA05532.

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.

Disclosure; Page 36; 52pp; English.

The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AA05532), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 583; DB 2; Length 583;

Best Local Similarity 100.0%; Pred. No. 7,3e-136; Mismatches 0; Gaps 0; Matches 583; Conservative 0; Indels 0; Gaps 0;

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QY 1 ATGGGAGCCCGAGCTGGGCCCCGAGACACAGGGGCTCTGGTGGGAGACTTTGAGTTAT 60
DB 1 ATGGGAGCCCGAGCTGGGCCCCGAGACACAGGGGCTCTGGTGGGAGACTTTGAGTTAT 60
QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCGGGGAGGGCCGAGAGCTGAC 120
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QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATAGATTGAGACCCGCTTCCGGCGAC 180
DB 121 CCGCTGCACCAAGCCATGCGGGCAGCTGAGATAGATTGAGACCCGCTTCCGGCGAC 180
QY 181 TTCTCTGATCTGGCGGCTCACTGATGATGACCCGAGCTCAGCCGAGCAAGCTTAC 240
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QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
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DB 301 CTCTTTGGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGGAACCACTGGTGG 360
QY 361 CAAGTGCAGAGAGTGTGATGTGTGCTTCAAGGAGACGGCGCTGTGATCAAGCAGC 420
DB 361 CAAGTGCAGAGAGTGTGATGTGTGCTTCAAGGAGACGGCGCTGTGATCAAGCAGC 420
QY 421 AGTGGGGGCTGGGGGAGGTTCACAGCTCTATACGGGGGAGCGGGCCCTGGAGAGCG 480
DB 421 AGTGGGGGCTGGGGGAGGTTCACAGCTCTATACGGGGGAGCGGGCCCTGGAGAGCG 480
QY 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGAAGCGGGGCGGTGG 540
DB 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGAAGCGGGGCGGTGG 540

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QY 541 GGGGCGCTGTAACTGTAGAGGCGCTTTTGTCTAGCAAGTGA 583
 Db 541 GGGGCGCTGTAACTGTAGAGGCGCTTTTGTCTAGCAAGTGA 583

RESULT 3
 ABV78153
 ID ABV78153 standard; DNA; 582 BP.

AC ABV78153;

DT 15-NOV-2002 (first entry)

DE Human bcl-w DNA SEQ ID NO 37.

KW RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;

KW virucide; protozoacide; gene; ds.

OS Homo sapiens.

PN W0200255693-42.

PD 18-JUL-2002.

PF 03-JAN-2002; 2002MO-EP000152.

PR 09-JAN-2001; 2001DE-01000586.

PR 26-OCT-2001; 2001DE-01055280.

PR 29-NOV-2001; 2001DE-01058411.

PR 07-DEC-2001; 2001DE-01060151.

XX (RIBO-) RIBOPHARMA AG.

PI Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX WPI; 2002-590671/63.

PT Inhibiting expression of target gene, useful e.g. for inhibiting

XX target and having an overhang.

XX Claim 10; Page 134; 203pp; German.

XX The invention relates to inhibiting expression of a target gene (I) in a

XX cell by introducing an inhibitory RNA (dsRNA) having a double-stranded

XX structure of at most 49 consecutive bases. At least part of one strand

XX (as1) of dsRNA is complementary to (i) and at least one end of dsRNA

XX has an overhang of 1-4 nucleotides. The method is used to inhibit the

XX expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.

XX in humans, also genes in Plasmodium or in viruses or viroids that are

XX pathogenic for humans, animals or plants. Introducing an overhang into

XX dsRNA greatly increases effectiveness for inhibiting gene expression,

XX both in vivo and in vitro and also increases stability and thus the

XX effective concentration inside the cell. The present sequence is that of

XX a gene related to the invention

XX

QY Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;

Best Local Similarity 99.5%; Pred. No. 2e-134;

Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCGGAGCCCGAGCTGCGCCCGAGACACAGCGGAGCTGTGACAGCTTTGTAGATTAT 60

Db 1 ATGCGGAGCCCGAGCTGCGCCCGAGACACAGCGGAGCTGTGACAGCTTTGTAGATTAT 60

QY 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGCGCCCGAGGAGGCCAGCAGCTGAC 120

Db 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGCGCCCGAGGAGGCCAGCAGCTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGGGAGCTGAGATGAGTGTGAGACCCGCTTCGGCGCAC 180

Db 121 CCGCTGCACCAAGCCATGCGGGGAGCTGAGATGAGTGTGAGACCCGCTTCGGCGCAC 180
 QY 181 TTCTCTGATCTGAGGAGCTCAAGCTCATGTGACCCAGAGCTCAGCCAGCAACGCTTAC 240
 Db 181 TTCTCTGATCTGAGGAGCTCAAGCTCATGTGACCCAGAGCTCAGCCAGCAACGCTTAC 240
 QY 241 CAGGCTTCGACGAACTTTTCAAGGAGGAGGCCCACTGGGGCCGCTTTGAGCTTTT 300
 Db 241 CAGGCTTCGACGAACTTTTCAAGGAGGAGGCCCACTGGGGCCGCTTTGAGCTTTT 300
 QY 301 CTCTTTGGGCGCTGACGTGTGCTGAGAGTGTCAACAGAGAGATGAAACCACTGTGGGA 360
 Db 301 GTCTTTGGGCGCTGACGTGTGCTGAGAGTGTCAACAGAGAGATGAAACCACTGTGGGA 360
 QY 361 CAAGTGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 CAAGTGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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 Db 421 AGTGGGAGCTGGGAGGAGTTCACAGCTCTATACGGGAGCGGGGCTGTGAGAGGCGCG 480
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 QY 541 GGGGCGCTGTAACTGTAGAGGCGCTTTTGTCTAGCAAGTGA 582
 Db 541 GGGGCGCTGTAACTGTAGAGGCGCTTTTGTCTAGCAAGTGA 582

RESULT 4

AE235729

ID AB235729 standard; DNA; 582 BP.

AC AB235729;

DT 07-FEB-2003 (first entry)

DE Human bcl-w polynucleotide SEQ ID NO 37.

KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;

KW protozoacide; gene expression; antisense; tumour; infection; Plasmodium;

KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;

KW Hepatitis C virus; human papilloma virus; gene; ds.

OS Homo sapiens.

PN DE10100588-A1.

PD 18-JUL-2002.

PF 09-JAN-2001; 2001DE-01000588.

PR 09-JAN-2001; 2001DE-01000588.

XX (RIBO-) RIBOPHARMA AG.

PI Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX WPI; 2002-683450/74.

PT Inhibiting expression of target genes, useful e.g. for treating tumors,

XX by introducing into cells two double-stranded RNAs that are complementary

XX to the target.

XX Claim 13; Page 30-31; 100pp; German.

XX The invention relates to inhibiting expression of a target gene in a cell

XX by introducing at least two oligonucleotides (dsRNA and II), both

XX with a double-stranded (ds) structure of at most 49 sequential nucleotide

XX pairs. At least part of one strand (S1, S2) of the ds structures in each

XX of dsRNA and II are complementary to regions in the target gene. The

CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by plasmid or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
CC

Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;

Best Local Similarity 99.5%; Pred. No. 2e-134;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ATGGGAGACCCGAGCTCGGCCCCGAGACACAGGGGCTCTGGTGGCAGACTTTGATGTTAT 60
DB 1 ATGGGAGACCCGAGCTCGGCCCCGAGACACAGGGGCTCTGGTGGCAGACTTTGATGTTAT 60
QY 61 AAGCTGAGGAGAGAGAGGTTATGTTGTTGAGAGTGGCCCCGGGAGAGGCCAGAGCTGAC 120
DB 61 AAGCTGAGGAGAGAGGTTATGTTGTTGAGAGTGGCCCCGGGAGAGGCCAGAGCTGAC 120
QY 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGAGTGAAGTTCGAGACCCGCTTCGGCGGACC 180
DB 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGAGTGAAGTTCGAGACCCGCTTCGGCGGACC 180
QY 181 TTCTGTGATCTGGCGGCTGAGTGTGATGATCCCAAGGCTAGCCACAGCAAGCTTCAAC 240
DB 181 TTCTGTGATCTGGCGGCTGAGTGTGATGATCCCAAGGCTAGCCACAGCAAGCTTCAAC 240
QY 241 CAGGCTCCGAGCACTTTTTCAGAGGGGGCCCCCAACTGGGGCCGCTTGATGCTTCTT 300
DB 241 CAGGCTCCGAGCACTTTTTCAGAGGGGGCCCCCAACTGGGGCCGCTTGATGCTTCTT 300
QY 301 CTCTTTGGGGCTGACACTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGATGAGGA 360
DB 301 GTCTTTGGGGCTGACACTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGATGAGGA 360
QY 361 CAAGTGAAGAGTGAATGATGCTTACCTGAGAGAGCGGCTGTGATGATTCACAGC 420
DB 361 CAAGTGAAGAGTGAATGATGCTTACCTGAGAGAGCGGCTGTGATGATTCACAGC 420
QY 421 AGTGGGGGCTGGCGGAGTTTCAACAGCTCTATACGGGAGACGGGGCCCTTGAAGAGCGCGG 480
DB 421 AGTGGGGGCTGGCGGAGTTTCAACAGCTCTATACGGGAGACGGGGCCCTTGAAGAGCGCGG 480
QY 481 CGCTGCGGAGAGGAGAACTGGGCGATCAGTGAAGGACAGTGTGACGGGGCCCTGAGCACTG 540
DB 481 CGCTGCGGAGAGGAGAACTGGGCGATCAGTGAAGGACAGTGTGACGGGGCCCTGAGCACTG 540
QY 541 GGGGCGCTGTAACTGATGAGGGGCTTTTGTCTAACAAGTGA 582
DB 541 GGGGCGCTGTAACTGATGAGGGGCTTTTGTCTAACAAGTGA 582
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RESULT 5
ABX09972
ID ABX09972 standard; DNA; 582 BP.

XX ABX09972;

XX 23-JAN-2003 (first entry)

DE Human bcl-w DNA fragment SEQ ID 37.

XX Oligonucleotide; interferon; oncogene; cytokine; id; developmental;

XX prion; inhibition; human; de.

XX Homo sapiens.

PN DE10100587-C1.

XX 21-NOV-2002.

XX 09-JAN-2001; 2001DE-01000587.

XX 09-JAN-2001; 2001DE-01000587.

XX (RIBO-) RIBOPHARMA AG.

XX Kreutzer R, Limmer S, Rost S, Hadwiger P;

XX WPI; 2002-742209/81.

XX Inhibiting expression of target genes, e.g. oncogenes, in cells, by

XX introduction of complementary double-stranded oligonucleotide, after

XX treating the cell with interferon.

XX This invention describes a novel method for inhibiting expression of a

XX target gene by introducing into the cell that contains the target gene at

XX least one oligonucleotide (dsRNA) that has a double-stranded (ds)

XX structure of not more than 49 consecutive nucleotides (nt), where at

XX least a segment of one strand of the ds structure is complementary with

XX the target gene and the cells are treated with interferon before

XX introduction of dsRNA. The method is used to inhibit expression of

XX target genes, particularly oncogenes, cytokine genes, id (not defined)

XX protein genes; developmental or prion genes; or genes expressed in

XX pathogenic organisms (particularly plasmids) or in viruses or viroids

XX (pathogenic in humans, animals or plants). Treating the cells with

XX interferon greatly increases the extent to which dsRNA can inhibit

XX expression of the target genes, and the effect is even greater when dsRNA

XX gene fragments used to illustrate the method of the invention

XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

XX Query Match 99.0%; Score 577.2; DB 6; Length 582;

XX Best Local Similarity 99.5%; Pred. No. 2e-134;

XX Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ATGGGAGACCCGAGCTCGGCCCCGAGACACAGGGGCTCTGGTGGCAGACTTTGATGTTAT 60
DB 1 ATGGGAGACCCGAGCTCGGCCCCGAGACACAGGGGCTCTGGTGGCAGACTTTGATGTTAT 60
QY 61 AAGCTGAGGAGAGAGGTTATGTTGTTGAGAGTGGCCCCGGGAGAGGCCAGAGCTGAC 120
DB 61 AAGCTGAGGAGAGAGGTTATGTTGTTGAGAGTGGCCCCGGGAGAGGCCAGAGCTGAC 120
QY 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGAGTGAAGTTCGAGACCCGCTTCGGCGGACC 180
DB 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGAGTGAAGTTCGAGACCCGCTTCGGCGGACC 180
QY 181 TTCTGTGATCTGGCGGCTGAGTGTGATGATCCCAAGGCTAGCCACAGCAAGCTTCAAC 240
DB 181 TTCTGTGATCTGGCGGCTGAGTGTGATGATCCCAAGGCTAGCCACAGCAAGCTTCAAC 240
QY 241 CAGGCTCCGAGCACTTTTTCAGAGGGGGCCCCCAACTGGGGCCGCTTGATGCTTCTT 300
DB 241 CAGGCTCCGAGCACTTTTTCAGAGGGGGCCCCCAACTGGGGCCGCTTGATGCTTCTT 300
QY 301 CTCTTTGGGGCTGACACTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGATGAGGA 360
DB 301 GTCTTTGGGGCTGACACTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGATGAGGA 360
QY 361 CAAGTGAAGAGTGAATGATGCTTACCTGAGAGAGCGGCTGTGATGATTCACAGC 420
DB 361 CAAGTGAAGAGTGAATGATGCTTACCTGAGAGAGCGGCTGTGATGATTCACAGC 420
QY 421 AGTGGGGGCTGGCGGAGTTTCAACAGCTCTATACGGGAGACGGGGCCCTTGAAGAGCGCGG 480
DB 421 AGTGGGGGCTGGCGGAGTTTCAACAGCTCTATACGGGAGACGGGGCCCTTGAAGAGCGCGG 480
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Qy 481 CGTCTGCGGGAGGGGAACTGGGCGATATGATGAGAGAGAGCTGACGGGGGGCCGTGGCACTG 540

Db 481 CGTCTGCGGGAGGGGAACTGGGCGATATGATGAGAGAGAGCTGACGGGGGGCCGTGGCACTG 540

Qy 541 GGGGCCCTGGTAACTGTAGGGGCGCTTTTTCGTACGAAGTGA 582

Db 541 GGGGCCCTGGTAACTGTAGGGGCGCTTTTTCGTACGAAGTGA 582

RESULT 6
ABL91694
ID ABL91694 standard; DNA; 582 BP.

DT 28-MAY-2002 (first entry)

	Human polynucleotide SEQ ID NO 37.
DE	

KM Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KM Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KM cytostatic; virucide; protozoacide; antibacterial; ds.

Homo sapiens.

PN DE10100586-C1.

PD 11-APR-2002.

PF 09-JAN-2001; 2001DE-01000586.

PR 09-JAN-2001; 2001DE-01000586.

PA (RIBO-) RIBOPHARMA AG.

PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
vv

DR WPI; 2002-270454/32.

PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT introducing double-stranded complementary oligonucleotides having unpaired
PT terminal bases.

PS Claim 13; Page 32; 104pp; German.

CC The invention relates to a method for inhibiting expression of a target
CC gene (ABU91658-ABU91797) in a cell by introducing at least one
CC oligonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one and a single-
CC stranded segment of 1-4 nt. The method provides oligonucleotides for
CC antisense inhibition of gene expression useful e.g. for treating tumours
CC but the oligonucleotides may also be directed against genes present
CC in pathogens (e.g. Plasmodium or viruses), viroid, pathogenic or prion genes,
CC animals or plants) or against cytokine, id, developmental or prion genes.
CC The method provides more effective inhibition of gene expression than use
CC of known oligonucleotides, probably because the uprated overhang
CC increases stability and thus intracellular concentration

SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match	99.0%	Score 577.2	DB 6	Length 582
Best Local Similarity	99.5%	Pred. No. 2e-134		
Matches 579	Conservative	0	Mismatches 3	Indels 0
				Gaps 0

QY 1 ATGGCGACCCGACGCTCGGCCCCAGACACAGGGGCTCGGTGGCGACACTTTGTATGGTTAT 60

Db 1 ATGGCGACCCGACGCTCGGCCCCAGACACAGGGGCTCGGTGGCGACACTTTGTATGGTTAT 60

QY 61 AAGCTGAGGAGAAAGGTTATGTCTGTGTGAGAGCTGGCCCCGGGAGAGGCCACAGAGCTTAC 120

Db 61 AAGCTGAGGAGAAAGGTTATGTCTGTGTGAGAGCTGGCCCCGGGAGAGGCCACAGAGCTTAC 120

QY 12 CCCTGACCAAGACCATGGGAGCACTGGATGAGTATGATTCGAGACCCGCTTCCGGCGACC 180

Db 121 CCGGTGACCAAGCCATGCGGAGCACTGGATGATGATTTCCAGACCCCGCTTCCGGCGACC 180

QY 181 TTCTGTGATCTGGCGGCTCAGCTCAGTGCATGTGACCCAGGCTCAGGCCACGACTTCAAC 240

Db 181 TTCTGTGATCTGGCGGCTCAGCTCAGTGCATGTGACCCAGGCTCAGGCCACGACTTCAAC 240

241 CAGGTCTCGACGAATTTTCAAGGGGGCCCAACGAGGGCGCCTTGGAGCCTTCTTT 300
 241 CAGGTCTCGACGAATTTTCAAGGGGGCCCAACGAGGGCGCCTTGGAGCCTTCTTT 300

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481 **CCTCCTCCGCGGCACATCCGGCAAGTGAAGGGGCCGTGTCATTG** **540**

481 CGTTCGCGGACGCGGACCTTGGGCTATCAATTGAGGACAGTGCTGACGGGCGCGTGCACTG 540

541 GGGGACCTTGTAACCTGTAGGGGACCTTJTJTGCTAGCAAGTGA 582

Db 541 GGGCCCTGGTAACTGTAGGGCCCTTTTTCCTAGCAAGTGA 582

RESULT 7
ABT166A3

AB116642 standard; DNA; 3542 bp

AC AB116642
XX

DI 03-APR-2003 (LIBL ENCLY)

DE HUMAIN DCI-2 gène sex LD NO 3.
XX

radiation therapy; catalytic domain; enzyme; human; ds.
NM HLI-1 camouar, DNAzyme, bcl-2 gene, camouar, mdr1gnauc, ccrnccncc-2
KW

Homo sapiens.

PN WO200299090-A1

PD 12-DEC-2002.

PF 07-JUN-2002; 2002WO-AU000739.

PR 07-JUN-2001; 2001AU-00005527.

PA (JOHU) JOHNSON & JOHNSON RES PTY LTD.

PI Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR,

DR WPI; 2003-140617/13.

Novel DNAzyme useful for treating tumors, and for enhancing the sensitivity of malignant or virus infected cells to therapy, comprises a catalytic domain and binding domain contiguous to the catalytic domain.

CC The invention relates to a DNzyme which specifically cleaves mRNA
CC transcribed from a member of the *bol-2* gene family. The DNzymes comprise
CC a catalytic domain, binding domains contiguous with the 5' and 3' end of
CC the catalytic domain, and therefore hybridize with, the two regions
CC immediately flanking the purine residue of the cleavage site within the

CC bcl-2 gene family mRNA, at which DNase-catalysed cleavage is desired. A
 CC pharmaceutical composition comprising a DNase of the invention is
 CC useful for treating tumours in a subject, and for enhancing the
 CC sensitivity of malignant or virus infected cells to infection
 CC therapy. The DNases are useful in diagnostics, therapeutics,
 CC prophylaxis, research agents and in kits. The DNases are also useful
 CC for increasing the susceptibility of tumour cells to anti-tumour
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide
 CC sequence represents a human bcl-2 gene of the invention

XX Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Query Match 98.6%; Score 575; DB 7; Length 3542;

Best Local Similarity 99.1%; Pred. No. 1.1e-133;
 Matches 578; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGGGAACCCGCTTGGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGTTAT 60
 DB 177 ATGGGGAACCCGCTTGGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGTTAT 236
 QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGCAGCTGAC 120
 DB 237 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGCAGCTGAC 296
 QY 121 CCGCTGACACCAAGCCATGCGGCGACGCTGAGATGATGATGACCCCGCTTCCGGCGCAC 180
 DB 297 CCGCTGACACCAAGCCATGCGGCGACGCTGAGATGATGATGACCCCGCTTCCGGCGCAC 356
 QY 181 TTCTCTGATCTGGCGGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 357 TTCTCTGATCTGGCGGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 416
 QY 241 CAGGCTCCGAGGAACTTTTCAAGGGGCCCCCACTGCGGCGCTTGTAGCTTCTTT 300
 DB 417 CAGGCTCCGAGGAACTTTTCAAGGGGCCCCCACTGCGGCGCTTGTAGCTTCTTT 476
 QY 301 CTCTTTGGGAGTCACTGTGTGCTGAGATGTCAACAGAGATGAAACCACTGGTGGGA 360
 DB 477 GTCTTTGGGAGTCACTGTGTGCTGAGATGTCAACAGAGATGAAACCACTGGTGGGA 536
 QY 361 CAACTGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 537 CAACTGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
 QY 421 AAGTGGGAGTGGGCGGAGTTCAAGCTCTATACGGGGAAGGGCCCTTGAAGAGCGCGG 480
 DB 597 AAGTGGGAGTGGGCGGAGTTCAAGCTCTATACGGGGAAGGGCCCTTGAAGAGCGCGG 656
 QY 481 CGTCTGCGGAGGAGGAACTGGGCGATCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 657 CGTCTGCGGAGGAGGAACTGGGCGATCAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 716
 QY 541 GGGGCGCTGTACTGATGAGGAGGCTTTTGTAGCAAGTGA 583
 DB 717 GGGGCGCTGTACTGATGAGGAGGCTTTTGTAGCAAGTGA 759

RESULT 8
 AAX25132
 ID AAX25132 standard; DNA; 581 BP.

XX AAX25132;
 AC 05-JUL-1999 (first entry)
 DT XX Human bcl-2 gene.
 DE XX
 KW Spermatogenesis; bcl-2 gene; Bcl-2; human; fertility; infertility;
 XX animal model; ss.
 OS Homo sapiens.
 XX
 PN W0913710-A1.

XX 25-MAR-1999.
 PD 16-SEP-1998; 98W0-AU000764.
 XX 16-SEP-1997; 97AU-00009228.
 PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Cory S, Adams J, Print C, Gibson J, Koentgen F;
 PI WPI; 1999-243890/20.
 DR P-PSDB; AAY05530.
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS Claim 3; Page 32; 52pp; English.

XX The present sequence is the human bcl-w gene encoding Bcl-w protein (see
 CC AAY05530), a pro-survival member of the Bcl-2 family which is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation in at least one
 CC allele of the human or murine bcl-w gene or in a gene associated with bcl
 CC -w. Such animals have disorganised seminiferous tubules and are
 CC substantially infertile, but possess no other major abnormalities as
 CC determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility

XX Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;

Query Match 98.3%; Score 573; DB 2; Length 581;

Best Local Similarity 99.1%; Pred. No. 2.3e-133;
 Matches 576; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGGGAACCCGCTTGGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGTTAT 60
 DB 1 ATGGGGAACCCGCTTGGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGTTAT 60
 QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGCAGCTGAC 120
 DB 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGCAGCTGAC 120
 QY 121 CCGCTGACACCAAGCCATGCGGCGACGCTGAGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 CCGCTGACACCAAGCCATGCGGCGACGCTGAGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 TTCTCTGATCTGGCGGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 TTCTCTGATCTGGCGGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 CAGGCTCCGAGGAACTTTTCAAGGGGCCCCCACTGCGGCGCTTGTAGCTTCTTT 300
 DB 241 CAGGCTCCGAGGAACTTTTCAAGGGGCCCCCACTGCGGCGCTTGTAGCTTCTTT 300
 QY 301 CTCTTTGGGAGTCACTGTGTGCTGAGATGTCAACAGAGATGAAACCACTGGTGGGA 360
 DB 301 GTCTTTGGGAGTCACTGTGTGCTGAGATGTCAACAGAGATGAAACCACTGGTGGGA 360
 QY 361 CAACTGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 CAACTGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 421 AAGTGGGAGTGGGCGGAGTTCAAGCTCTATACGGGGAAGGGCCCTTGAAGAGCGCGG 480
 DB 421 AAGTGGGAGTGGGCGGAGTTCAAGCTCTATACGGGGAAGGGCCCTTGAAGAGCGCGG 480

QY 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
 DB 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
 QY 541 GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGTG 581
 DB 541 GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTCTAGCAAGTGTG 581

RESULT 9

AAV28334
 ID AAV28334 standard; cDNA; 579 BP.

AAV28334;
 AC AAV28334;

DT 02-OCT-1998 (first entry)

DE Human bcl-2 gene.

XX ss; bcl-2; bcl-2; cell death pathway; apoptotic; apoptosis; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..579

FT /*tag= a

FT /product= "bcl-2"

FT /note= "No stop codon given"

XX US5789201-A.

XX 04-AUG-1998.

XX 11-FEB-1997; 97US-00798897.

XX 23-FEB-1996; 96US-0012201P.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI; 1998-446079/38.

XX P-PSDB; AAM61392.

XX Nucleic acid encoding B-cell lymphoma-2 protein - useful for producing

XX recombinant protein for use in treating uncontrolled cell growth e.g.

XX Claim 3; Column 15/16; 27pp; English.

XX The mammalian bcl-2 genes encode a protein that is a member of the bcl-2
 CC family; components in the cell death pathway. The bcl-2 family have both
 CC apoptotic activity and the apoptosis blocking activity. bcl-2 falls in
 CC the apoptosis activity category. The recombinant protein may be used to
 CC prevent uncontrolled cell growth, either by its direct administration to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired

XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

XX Query March 97.44; Score 567.8; DB 2; Length 579;

XX Best Local Similarity 90.88; Pred. No. 4.5e-132;

XX Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGGCTGAGCCGAGACAGAGGAGCTGTGAGGAGCTTTGAGGTTAT 60

DB 1 ATGGCGACCCAGGCTGAGCCGAGACAGAGGAGCTGTGAGGAGCTTTGAGGTTAT 60

QY 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGAGCCCGGAGAGGGCCAGCAGCTGAC 120

DB 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGCTGAGCCCGGAGAGGGCCAGCAGCTGAC 120

QY 121 CCAGTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTCAGACCCGCTTCCGGCGCAC 180
 DB 121 CCAGTGCACCAAGCCATGCGGGCAGCTGAGATGAGTTCAGACCCGCTTCCGGCGCAC 180
 QY 181 TTCTGTGATCTGCGGCTGAGCTGATGATGACCCAGGCTCAAGCCAGCAAGCTTCAAC 240
 DB 181 TTCTGTGATCTGCGGCTGAGCTGATGATGACCCAGGCTCAAGCCAGCAAGCTTCAAC 240
 QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTGTAGCCTTTCTT 300
 DB 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTGTAGCCTTTCTT 300
 QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGATGTCACAAAGAGATGGAACCACTGGTGGGA 360
 DB 301 GTCTTTGGGGCTGCACTGTGTGCTGAGATGTCACAAAGAGATGGAACCACTGGTGGGA 360
 QY 361 CAAGTGCAGAGATGATGATGATGAGCTTACCTGAGACCGCGCTGTGACTGATCCACAGC 420
 DB 361 CAAGTGCAGAGATGATGATGATGAGCTTACCTGAGACCGCGCTGTGACTGATCCACAGC 420
 QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGGAACGGGCGCTGGAGAGCGCGG 480
 DB 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGGAACGGGCGCTGGAGAGCGCGG 480
 QY 481 CGTCTCGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
 DB 481 CGTCTCGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540
 QY 541 GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTCTAGCAAG 579
 DB 541 GGGGCCCTGTGTAAGTGTAGGGGCGCTTTTGTCTAGCAAG 579

RESULT 10

AAK15946
 ID AAK15946 standard; cDNA; 579 BP.

XX AAK15946;

XX 20-MAY-1999 (first entry)

XX cDNA encoding the human bcl-2 protein.

XX Rat bcl-2 protein; Bcl-2; human bcl-2 protein; Bcl-2 homologues;

XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;

XX head trauma; Alzheimer's Disease; neuronal; muscular degenerative disease;

XX multiple sclerosis; myocardial infarction; vitally induced cell death;

XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;

XX premature cell death; cell death stimulator; prolonged cell life span;

XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;

XX ss.

XX Homo sapiens.

XX US5883229-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-00978523.

XX 23-FEB-1996; 96US-0012201P.

XX 11-FEB-1997; 97US-00798897.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI; 1999-214150/18.

XX P-PSDB; AAM97392.

XX Novel bcl-2 homologues of the rat and human bcl-2 protein - useful for

XX modulating programmed cell death.

PS Disclosure; Col 15-16; 26pp; English.

XX The present sequence encodes human bcl-2 protein (Hbcl-2). The
XX specification also describes rat bcl-2 protein (Rbcl-2). Rbcl-2 and Hbcl-
CC y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-2 and
CC Hbcl-2 may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites

XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

SO Query Match 97.4%; Score 567.8; DB 2; Length 579;
Best Local Similarity 98.8%; Pred. No. 4,5e-122;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGACCTCGGCCGACACACAGCGGCTCTGTGGAGACTTTGTAGTTAT 60
DB 1 ATGGCGACCCGACCTCGGCCGACACACAGCGGCTCTGTGGAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGCGAAGGTTATGTCTGTGGAGCTGGCCCGGGGAGGCGCCAGAGCTGAC 120
DB 61 AAGCTGAGGCGAAGGTTATGTCTGTGGAGCTGGCCCGGGGAGGCGCCAGAGCTGAC 120
QY 121 CCGCTGACACCAAGCCATCGGCGAGCTGAGATGATGAGATCCGCTTCGCGGAGCC 180
DB 121 CCGCTGACACCAAGCCATCGGCGAGCTGAGATGATGAGATCCGCTTCGCGGAGCC 180
QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCCGAGCTCAGCCAGCAAGCTTACC 240
DB 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCCGAGCTCAGCCAGCAAGCTTACC 240
QY 241 CAGGCTCTCGAGTAACTTTTCAGGGGCGCCCACTGGGCGCTTGTAGCTTCTTT 300
DB 241 CAGGCTCTCGAGTAACTTTTCAGGGGCGCCCACTGGGCGCTTGTAGCTTCTTT 300
QY 301 CTCTTGGGGGCTGCACTGTGTCTGAGAGTGTCAACAGAGATGAAACCACTGATGGA 360
DB 301 CTCTTGGGGGCTGCACTGTGTCTGAGAGTGTCAACAGAGATGAAACCACTGATGGA 360
QY 361 CAGTGTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CAGTGTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGGAACGGGGCCCTTGAAGAGCGGG 480
DB 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATACGGGGAACGGGGCCCTTGAAGAGCGGG 480
QY 481 CGTCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 CGTCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 GGGGCGCTGTACTGTAGAGGCGCTTTTGTAGCAAG 579
DB 541 GGGGCGCTGTACTGTAGAGGCGCTTTTGTAGCAAG 579

RESULT 11
ADBS2996
ID ADBS2996 standard; DNA; 582 BP.
XX AC ADBS2996;

XX 04-DEC-2003 (first entry)

XX Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.

DE toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;

XX toxicity marker; toxicity progression; drug screening;

XX primary rat hepatocyte toxicity modelling; gene; ds.

XX Rattus norvegicus.

PN W02003065993-A2.

XX 14-AUG-2003.

XX 04-FEB-2003; 2003WO-US003482.

PR 04-FEB-2002; 2002US-0353171P.

PR 13-MAR-2002; 2002US-0363534P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 10-APR-2002; 2002US-0371150P.

PR 11-APR-2002; 2002US-0374113P.

PR 19-APR-2002; 2002US-0373601P.

PR 19-APR-2002; 2002US-0373602P.

PR 22-APR-2002; 2002US-0374139P.

PR 08-MAY-2002; 2002US-0376370P.

PR 09-MAY-2002; 2002US-0376652P.

PR 09-MAY-2002; 2002US-0376653P.

PR 09-MAY-2002; 2002US-0376655P.

PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.

PR 04-SEP-2002; 2002US-0407688P.

PR 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

PA Mendick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

PI Elashoff M;

XX WPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for

PT identifying hepatotoxic compounds, comprises comparing a gene expression

PT profile of a tissue or cell sample to a database of Tox mean and non-Tox

PT mean values.

XX Claim 44; SEQ ID NO 3538; 874p; English.

XX The present invention describes a method for determining whether a

CC compound induces a toxic effect on a tissue or cell. The method comprises

CC preparing a gene expression profile of a tissue or cell sample exposed to

CC the compound, and comparing the gene expression profile to a database

CC comprising data or information on the Tox mean and non-Tox mean value.

CC The method is useful for predicting or identifying at least one toxic

CC effect, particularly hepatotoxicity, of a test or unknown compound. The

CC genes listed in the specification are useful as diagnostic or toxicity

CC markers for the prediction or identification of the physiological state

CC of tissue or cell sample that has been exposed to a compound, or to

CC identify or predict the toxic effects of a compound or an agent. These

CC may also be used as markers for monitoring toxicity progression or for

CC drug screening. The present sequence represents a primary rat hepatocyte

CC toxicity modelling related gene sequence from the present invention.

XX Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

SO Query Match 90.5%; Score 527.6; DB 9; Length 582;
Best Local Similarity 94.2%; Pred. No. 5e-122;
Matches 546; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGACCTCGGCCGACACACAGCGGCTCTGTGGAGACTTTGTAGTTAT 60


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Db      1  ATGGGACCCCGAGCTCAACCCGACACACAGGGCTCTAGTGTGCTGACTTTGTAGGCTAT 60
QY      61  AAGCTGAGGCGAAGAGGTTATGTGTGAGACTGCCCCGGGGAGGGCCGACAGCTGAC 120
Db      61  AAGCTGAGGCGAAGAGGTTATGTGTGAGACTGCCCCGGGGAGGGCCGACAGCTGAC 120
QY      121  CCGGTGACCAAGGCATGCGGGGAGCTGAGATGATTCGAGACCCGCTTCCGGCGAC 180
Db      121  CCGGTGACCAAGGCATGCGGGGAGCTGAGATGATTCGAGACCCGCTTCCGGCGAC 180
QY      181  TTCTCTGATCTGCGGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAAGCTTAC 240
Db      181  TTCTCTGATCTGCGGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAAGCTTAC 240
QY      241  CAGGTCTCCGACGAATCTTTTCAAGGGGGCCCACTGGGGCGCTTGTAGCCCTTT 300
Db      241  CAGGTCTCCGACGAATCTTTTCAAGGGGGCCCACTGGGGCGCTTGTGTGGATTT 300
QY      301  CTCTTTGGGGCTGCACTGTGTGCTGAGAGTCAACAGAGATGAGACCACTGTGGGA 360
Db      301  GTCTTTGGGGCTGCTCTGTGTGCTGAGAGTGTCAACAGAGATGAGACCACTGTGGGA 360
QY      361  CAAGTGCAGAGTGGATGTGCTTACCTGAGACGGGGCTGTGCTGATTCACAGC 420
Db      361  CAAGTGCAGAGTGGATGTGCTTACCTGAGACGGGGCTGTGCTGATTCACAGC 420
QY      421  AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGAGACGGGGCCCTGAGAGAGCG 480
Db      421  AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGAGACGGGGCCCTGAGAGAGCG 480
QY      481  CGTCTGCGGAGGGGAACTGAGCATCAATGAGAGACAGTGTGACGGGGGCGTGGCA 540
Db      481  CGTCTGCGGAGGGGAACTGAGCATCAATGAGAGACAGTGTGACGGGGGCGTGGCA 540
QY      541  GGGGCGCTGTGTAAGTGAAGGGGCTTTTGTGCTAGCAAGTGA 582
Db      541  GGGGCGCTGTGTAAGTGAAGGGGCTTTTGTGCTAGCAAGTGA 582

RESULT 12
AAV28333 standard; cDNA; 579 BP.
ID      AAV28333
AC      AAV28333;
DT      02-OCT-1998 (first entry)
XX
DE      Rat bcl-y gene.
XX
KW      ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS      Rattus sp.
XX
FH      Key Location/Qualifiers
FT      CDS 1..579
FT      /tag= a
FT      /product= "bcl-y"
FT      /note= "No stop codon given"

US5789201-A.
XX
PN      04-AUG-1998.
XX
PF      11-FEB-1997; 97US-00798897.
XX
PR      23-FEB-1996; 96US-0012201P.
XX
PA      (COCE-) COCENSYS INC.
XX
PI      Guastella J;
XX
DR      WPI: 1998-446079/38.
DR      P-PSDB; AAM61391.

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XX      XX
PT      Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT      recombinant protein for use in treating uncontrolled cell growth e.g.
PT      cancers.
PS      Claim 2; Column 13/14; 27pp; English.
XX      CC
XX      The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX      CC family, components in the cell death pathway. The bcl-2 family have both
XX      CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in
XX      CC the apoptosis activity category. The recombinant protein may be used to
XX      CC prevent uncontrolled cell growth, either by its direct administration to
XX      CC recombinant genetic constructs to increase its expression in vivo. Also,
XX      CC antisense constructs can be used in disorders where prevention of cell
XX      CC death is desired
SQ      Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

Query Match      89.7%; Score 523; DB 2; Length 579;
Best Local Similarity 94.0%; Pred. No. 7e-121;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY      1  ATGGGACCCCGAGCTCAACCCGACACACAGGGCTCTAGTGTGCTGACTTTGTAGGCTAT 60
Db      1  ATGGGACCCCGAGCTCAACCCGACACACAGGGCTCTAGTGTGCTGACTTTGTAGGCTAT 60
QY      61  AAGCTGAGGCGAAGAGGTTATGTGTGAGACTGCCCCGGGGAGGGCCGACAGCTGAC 120
Db      61  AAGCTGAGGCGAAGAGGTTATGTGTGAGACTGCCCCGGGGAGGGCCGACAGCTGAC 120
QY      121  CCGGTGACCAAGGCATGCGGGGAGCTGAGATGATTCGAGACCCGCTTCCGGCGAC 180
Db      121  CCGGTGACCAAGGCATGCGGGGAGCTGAGATGATTCGAGACCCGCTTCCGGCGAC 180
QY      181  TTCTCTGATCTGCGGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAAGCTTAC 240
Db      181  TTCTCTGATCTGCGGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAAGCTTAC 240
QY      241  CAGGTCTCCGACGAATCTTTTCAAGGGGGCCCACTGGGGCGCTTGTAGCCCTTT 300
Db      241  CAGGTCTCCGACGAATCTTTTCAAGGGGGCCCACTGGGGCGCTTGTAGCCCTTT 300
QY      301  CTCTTTGGGGCTGCACTGTGTGCTGAGAGTCAACAGAGATGAGACCACTGTGGGA 360
Db      301  GTCTTTGGGGCTGCTCTGTGTGCTGAGAGTGTCAACAGAGATGAGACCACTGTGGGA 360
QY      361  CAAGTGCAGAGTGGATGTGCTTACCTGAGACGGGGCTGTGCTGATTCACAGC 420
Db      361  CAAGTGCAGAGTGGATGTGCTTACCTGAGACGGGGCTGTGCTGATTCACAGC 420
QY      421  AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGAGACGGGGCCCTGAGAGAGCG 480
Db      421  AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGAGACGGGGCCCTGAGAGAGCG 480
QY      481  CGTCTGCGGAGGGGAACTGAGCATCAATGAGAGACAGTGTGACGGGGGCGTGGCA 540
Db      481  CGTCTGCGGAGGGGAACTGAGCATCAATGAGAGACAGTGTGACGGGGGCGTGGCA 540
QY      541  GGGGCGCTGTGTAAGTGAAGGGGCTTTTGTGCTAGCAAGTGA 579
Db      541  GGGGCGCTGTGTAAGTGAAGGGGCTTTTGTGCTAGCAAG 579

RESULT 13
AAV15945 standard; cDNA; 579 BP.
ID      AAV15945
AC      AAV15945;
DT      20-MAY-1999 (first entry)
XX
DE      CDNA encoding the rat bcl-y protein.

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KM	Rat bcl-y protein; Bcl-Y; human bcl-y protein; Hbcl-Y; bcl-2 homologue;
KM	programmed cell death; apoptosis; neurosis; cell death inhibitor; stroke;
KM	head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM	multiple sclerosis; myocardial infarction; vitally induced cell death;
KM	aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM	premature cell death; cell death stimulator; prolonged cell life span;
KM	Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
KM	se.
OS	Rattus sp.
XX	
PN	U55883229-A.
PD	16-MAR-1999.
XX	
PF	25-NOV-1997; 97US-00978523.
XX	
PR	23-FEB-1996; 96US-0012201P.
XX	
PR	11-FEB-1997; 97US-00798897.
XX	
PA	(COCE-) COCENSYS INC.
XX	
PI	Guastella J;
XX	
DR	WPI: 1999-214150/18.
DR	P-PSDB; AAM97391.
XX	
PT	Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT	modulating programmed cell death.
XX	
PS	Disclosure; Col 13-16; 26pp; English.
XX	
CC	The present sequence encodes rat bcl-y protein (bcl-y). The
CC	specification also describes human bcl-y protein (Hbcl-y). Bcl-y and
CC	Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC	programmed cell death (apoptosis and neurosis). Bcl-y and Hbcl-y
CC	proteins may be used to treat conditions associated with a disruption of
CC	the cell death pathway. If they act as cell death inhibitors, they may be
CC	used in therapies to treat subjects suffering from: strokes, head trauma,
CC	Alzheimer's Disease, neural and muscular degenerative diseases
CC	(especially multiple sclerosis), myocardial infarction, vitally induced
CC	cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC	- conditions where cells under go premature cell death as a result of
CC	triggers which may or may not be apparent. They may also be used in this
CC	way to develop cell lines which remain viable in culture for an extended
CC	period. In contrast, if they act as cell death stimulators, Bcl-y and
CC	Hbcl-y may be used to treat conditions associated with prolonged cell
CC	life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC	and auto/hyperimmune diseases. They may also be used to cause cell death
CC	in, and hence control, parasites
XX	
XX	Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
XX	
Query Match	89.7%; Score 523; DB 2; Length 579;
Best Local Similarity	94.0%; Pred. No. 7e-121;
Matches 544; Conservative	0; Mismatches 35; Indels 0; Gaps 0
QY	1 ATGGCGAACCAGCTCTGGCCCCCAACACACAGGGCTCTGGTGGCAACTTTGAGTTAT 60
DB	1 ATGGCGAACCAGCTCTGAACCCCAACACACAGGGCTCTGAGGTGACTTTGAGTTAT 60
QY	61 AAGCTGAGCAGAGAGGTTATGTCGTGGAGCTGGCCCCGGGAGGAGCCACAGAGGTGAC 120
DB	61 AAGCTGAGCAGAGAGGTTATGTCGTGGAGCTGGCCCCGGGAGGAGCCACAGAGGTGAC 120
QY	121 CCGCTGACCAACAGCCATGCGGGCAGCTGGAGATGATGAGACCCGGCTTCGGGCGACCC 180
DB	121 CCGGTGACCAACAGCCATGCGGGCAGCTGGAGATGATGAGACCCGGCTTCGGGCGACCC 180
QY	181 TTCTCTGATGTGGCGGCTGACTGATGATGATGCCAGGCTAGCCCAAGCAAGCTTCACC 240
DB	181 TTCTCTGATGTGGCGGCTGACTGATGATGATGCCAGGCTAGCCCAAGCAAGCTTCACC 240

QY	241	CAGATCTCCAGCAAACTTTTTCAGAGGGAGCCCAAACTGGGGGCGCTTTGAGCCTTCTTT	300
Db	241	CAGATTTCCGACCAACTTTTCCAAAGGGAGCCCAAACTGGGGCGCTTTGAGCAATCTTT	300
QY	301	CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGAGATGAAACCACTGTGGGA	360
Db	301	GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCACTGTGGGA	360
QY	361	CAAGTGCAGAGATGTGATGTGTGGCTTACTTGAGAACGCGGCTGGTCACTGGATCCACAGC	420
Db	361	CAAGTGCAGAGATTGAGATGTGACCTTACTCTGAGACAGACGCTTGGTGACTGGATCCACAGC	420
QY	421	AGTGGGGGGCTGGGGCGGAGTTCAAGACCTTAAAGGGGACGGGGGCGCTGAGAGAGCGCGG	480
Db	421	AGTGGGGGGCTGGGGGGAGTTCAAGACTTCTTAAAGGGGACGGGGGCGCTGAGAGAGGACAGG	480
QY	481	CGTCTGCGGAGAGGGGAACTGAGGATCAGTAGAGGACAGTGTCTGACGGAGGCGCTGGCACTG	540
Db	481	CGTCTGCGGAGAGGGGAACTGAGGATCAGTAGAGGACAGTGTCTGACGGAGGCGCTGGCACTG	540
QY	541	GGGGCCCTGGTAACTGTAGGGGGCCTTTTGTCTGACAG	579
Db	541	GGGGCCCTGGTAACTGTAGGGGGCCTTTTGTCTGACAG	579
RESULT 14			
ID	AAAX25133	standard; DNA; 581 BP.	
AC	AAAX25133;		
XX			
DT	05-JUL-1999	(first entry)	
XX			
DE	Mouse bcl-w gene.		
XX			
KM	Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;		
KM	animal model; se.		
XX			
OS	Mus sp.		
PN	W09913710-A1.		
XX			
PD	25-MAR-1999.		
XX			
PF	16-SEP-1998; 98MO-AU000764.		
XX			
PR	16-SEP-1997; 97AU-00009228.		
XX			
PA	(HALL-) HALI INST MEDICAL RES WALTER & ELIZA.		
XX			
PI	Cory S, Adams J, Print C, Gibson L, Koentgen F;		
XX			
DR	WPI; 1999-243890/20.		
XX			
PT	P-PSDB; AAY05531.		
XX			
PS	Claim 3; Page 34; 52pp; English.		
CC	The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see		
CC	AAV05531), a pro-survival member of the Bcl-2 family which is widely		
CC	expressed and is essential for spermatogenesis. The invention		
CC	relates generally to a method of treatment and to an animal model for the		
CC	identification of molecules and genetic sequences useful for inducing or		
CC	reducing fertility of male animals. Methods are provided for the		
CC	treatment of infertility, or for reducing fertility, by modulating		
CC	spermatogenesis. An animal model carries a mutation, is at least one		
CC	allele of the human or murine bcl-w gene or in a gene associated with bcl		
CC	-w. Such animals have disorganised seminiferous tubules and are		
CC	substantially infertile, but possess no other major abnormalities as		
CC	determined by histological examination. They can be used to screen for		
CC	therapeutic molecules including genetic sequences capable of inducing,		

CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility

SO Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 89.5%; Score 521.8; DB 2; Length 581;
 Best Local Similarity 93.6%; Pred. No. 1.4e-120;
 Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGCTCGGCCGAGACACAGGGCTCTGTGGGAGACCTTTGATAGTTAT 60
 Db 1 ATGGCGACCCCGAGCTCGGCCGAGACACAGGGCTCTGTGGGAGACCTTTGATAGTTAT 60
 QY 61 AAGCTGAGGCGAAGGGTTATGCTGTGAGAGCTGGCCCCGGGGAGGSCCCAGACAGCTGAC 120
 Db 61 AAGCTGAGGCGAAGGGTTATGCTGTGAGAGCTGGCCCCGGGGAGGSCCCAGACAGCTGAC 120
 QY 121 CCGCTGCACCAAGGCATGCGGGGAGCTGGAGATGATTCGAGACCCGCTTCGGCGGAC 180
 Db 121 CCGCTGCACCAAGGCATGCGGGGAGCTGGAGATGATTCGAGACCCGCTTCGGCGGAC 180
 QY 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGCTCAGGCCAGACGCTTCACC 240
 Db 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGCTCAGGCCAGACGCTTCACC 240
 QY 241 CAGGTTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTTTGAGCCTTTT 300
 Db 241 CAGGTTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTTTGAGCCTTTT 300
 QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGACCACTGTGGGA 360
 Db 301 GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAGATGACCACTTTGTGGGA 360
 QY 361 CAAATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 CAAATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 421 AGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGGGAGGGGCTGAGAGAGGGGG 480
 Db 421 AGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGGGAGGGGCTGAGAGAGGGGG 480
 QY 481 CGTCTGCGGAGAGGGAATCTGGGCATCAGTGAAGAGACAGTGTGACGGGGGCGGTGGAC 540
 Db 481 CGTCTGCGGAGAGGGAATCTGGGCATCAGTGAAGAGACAGTGTGACGGGGGCGGTGGAC 540
 QY 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
 Db 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 15

AAT96578
 ID AAT96578 standard; DNA; 581 BP.

AC AAT96578;

DT 22-APR-1998 (first entry)

XX Mouse bcl-w DNA.

XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;

KW diagnosis; degenerative disease; ss.

OS Mus sp.

XX Location/Qualifiers

1..507

FT /*cag= a

FT /product= "bcl-w"

/note= "q"

XX MO9735971-A1.

PD 02-OCT-1997.

XX 27-MAR-1997; 97WO-AU000199.

XX 27-MAR-1996; 96AU-00008965.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Cory S, Adams JM, Gibson LM, Holmgren SF;

XX MPI; 1997-489635/45.

XX P-PSDB; AAM36048.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.

PS Claim 3; Page 50-51; 86pp; English.

CC This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
 CC family. This gene promotes cell survival, so its modulation is useful in
 CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
 CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
 CC hypoxia, ischaemia, human immunodeficiency virus infection or in cell
 CC transplants. Up-regulation of the gene can also be used to modify cell
 CC lines cultured in vivo, e.g. to develop new lines, to facilitate
 CC isolation of hybridomas and to increase survival of primary explants
 CC during genetic modification. It can be used to produce recombinant Bcl-w
 CC for therapy, diagnosis, antibody production or screening of potential
 CC modulators

SO Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;

Query Match 85.9%; Score 501; DB 2; Length 581;
 Best Local Similarity 91.4%; Pred. No. 2.2e-115;
 Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGGGACCCCGAGCTCGGCCGAGACACAGGGCTCTGTGGGAGACCTTTGATAGTTAT 60

Db 1 ATGGGACCCCGAGCTCGGCCGAGACACAGGGCTCTGTGGGAGACCTTTGATAGTTAT 60

QY 61 AAGCTGAGGCGAAGGGTTATGCTGTGAGAGCTGGCCCCGGGGAGGSCCCAGACAGCTGAC 120

Db 61 AAGCTGAGGCGAAGGGTTATGCTGTGAGAGCTGGCCCCGGGGAGGSCCCAGACAGCTGAC 120

QY 121 CCGCTGCACCAAGCCATCGGGCTGTGAGACGAGTTTGAAGACCCGTTCCGCGAC 180

Db 121 CCGCTGCACCAAGCCATCGGGCTGTGAGACGAGTTTGAAGACCCGTTCCGCGAC 180

QY 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGCTCAGGCCAGACGCTTCACC 240

Db 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGCTCAGGCCAGACGCTTCACC 240

QY 241 CAGGTTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTTTGAGCCTTTT 300

Db 241 CAGGTTCTCCGACGAACCTTTTCAAGGGGGCCCCCACTGGGGCCGCTTTGAGCCTTTT 300

QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGAGATGAAACAATGTTGGGA 360

Db 301 GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAGATGAAACAATGTTGGGA 360

QY 361 CAAAGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

Db 361 CAAAGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 421 AAGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGGGAGGGGCTGAGAGAGGGGCGGTGGAC 480

Db 421 AAGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGGGAGGGGCTGAGAGAGGGGCGGTGGAC 480

QY 481 CGTCTGCGGAGAGGGAATCTGGGCATCAGTGAAGAGACAGTGTGACGGGGGCGGTGGAC 540

Db 481 CGTCTGCGGAGAGGGAATCTGGGCATCAGTGAAGAGACAGTGTGACGGGGGCGGTGGAC 540

Qy 541 GGGGCCCTGTACTGTAGGGCCCTTTTGTGCTAGCAAGTG 581
|||
Db 541 GGGGCCCTGTACTGTAGGGGCCCTTTTGTGCTAGCAAGTG 581
|||

Search completed: March 29, 2004, 04:39:43
Job time : 369.622 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: March 25, 2004, 15:35:20 / Search time 36 Seconds
(without alignments)
1691.528 Million cell updates/sec

Title: US-09-155-327g-7
Perfect score: 1007
Sequence: 1 MATRPASAPDRALVADPVG.....LTGVALGALVTGAFPAK 193

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	98.9	193	11	088996
2	996	98.9	219	11	077860
3	996	94.9	193	11	08CG14
4	761	75.6	178	11	09CWM5
5	761	75.6	178	11	08CPR2
6	440.5	43.7	233	6	09MYW4
7	435.5	43.2	233	11	035844
8	433.5	43.0	233	6	08SQ42
9	431.5	42.9	233	6	09N142
10	428.5	42.6	233	6	09MZS7
11	413	41.0	236	11	08BCK4
12	413	41.0	236	11	07TSN8
13	403	40.0	238	11	090298
14	402	39.9	79	11	07TS61
15	401	39.8	180	6	09BD5
16	401	39.8	217	11	099N35

17	399	39.6	236	11	0923R6	Q923R6 cricetus
18	398.5	39.6	180	6	Q9BDX7	Q9BDX7 bos taurus
19	396.5	39.4	235	6	Q81008	Q81008 felis silve
20	380.5	37.8	284	11	Q7TS62	Q7TS62 ratius norv
21	374.5	37.2	188	11	Q9QW2	Q9QW2 mus musculu
22	374.5	37.2	235	11	Q35843	Q35843 mus musculu
23	373.5	37.1	188	4	Q9H1R6	Q9H1R6 homo sapien
24	373	37.0	204	13	Q902H2	Q902H2 xenopus lae
25	366.5	36.4	153	6	Q7YR86	Q7YR86 canis fami
26	354	35.2	185	6	Q8WJ81	Q8WJ81 bos taurus
27	347	34.5	219	11	Q99N36	Q99N36 mus musculu
28	343.5	34.1	199	11	Q8C5P0	Q8C5P0 mus musculu
29	296	29.4	89	13	Q8WJ1	Q8WJ1 gallus gall
30	189	18.8	209	11	Q9TK5	Q9TK5 ratius norv
31	185	18.4	170	11	Q9WJ5	Q9WJ5 ratius norv
32	184	18.3	209	11	Q8C264	Q8C264 mus musculu
33	176.5	17.5	192	13	Q919N4	Q919N4 brachydantio
34	175.5	17.4	190	4	Q8NFF3	Q8NFF3 homo sapien
35	171.5	17.0	221	13	Q98UJ3	Q98UJ3 xenopus lae
36	168.5	16.7	125	4	Q9H1R5	Q9H1R5 homo sapien
37	163	16.2	58	11	Q9R1B3	Q9R1B3 ratius norv
38	162	16.1	235	5	Q967D2	Q967D2 geodia cydo
39	159.5	15.8	163	6	Q9MZS6	Q9MZS6 ovis aries
40	155.5	15.4	173	11	Q8K3J2	Q8K3J2 mus musculu
41	153	15.2	173	4	Q8WZ49	Q8WZ49 homo sapien
42	153	15.2	173	11	Q9TKJ3	Q9TKJ3 ratius norv
43	152	15.1	67	6	Q8WJ83	Q8WJ83 cervus elap
44	148.5	14.7	218	5	Q9N754	Q9N754 suberites d
45	148	14.7	192	6	Q8SQ43	Q8SQ43 felis silve

ALIGNMENTS

RESULT 1

088996 PRELIMINARY; FRT; 193 AA.

AC 088996/

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE BCL-W.

GN Rattus norvegicus (Rat).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

OX [1]

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=2672518; PubMed=12787069;

RA Itoh T., Itoh A., Pleasure D.,

RT "Bcl-2-related protein family gene expression during oligodendroglial differentiation";

RT J. Neurochem. 85:1500-1512(2003).

RL EMBL: AF096291; AAC64200.1; -

DR EMBL: AY185096; AAC64468.1; -

DR HSSP: Q07817; IMAZ.

DR GO: GO:0006915; P:apoptosis regulator activity; IEA.

DR GO: GO:0006915; P:apoptosis; IEA.

DR InterPro: IPR00712; Bcl2_BH.

DR InterPro: IPR003093; Bcl2_BH.

DR InterPro: IPR002475; Bcl2_Family.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 98.9%; Score 996; DB 11; Length 193;
 Best Local Similarity 98.4%; Pred. No. 1.4e-80;

Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGGPRADPLHQMRAGDEFEFRRT 60
 DB 1 MATPASPTDTRALVADFGYKLRQKGYVCGAGPGGPRADPLHQMRAGDEFEFRRT 60
 QY 61 FSDLAQQLHTVTPGSAQQRFTQVSDLFQGGPNWGRVAFVFGALCAESVKNKEPVLVG 120
 DB 61 FSDLAQQLHTVTPGSAQQRFTQVSDLFQGGPNWGRVAFVFGALCAESVKNKEPVLVG 120
 QY 121 QVQEMWVAVLETRLADWIIHSSGGMAEFTALYDGDALBEARRLRSGNMAVRTVLTGAVAL 180
 DB 121 QVQDMWVAVLETRLADWIIHSSGGMAEFTALYDGDALBEARRLRSGNMAVRTVLTGAVAL 180
 QY 181 GALVTGAFPAK 193
 DB 181 GALVTGAFPAK 193

RESULT 2

Q7TS60 PRELIMINARY; PRT; 219 AA.

AC Q7TS60;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE BCL-WEL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RC MEDLINE=2672518; PubMed=12787069;
 RA Itoh T., Itoh A., Pleasure D.;
 RT "Bcl-2-related protein family gene expression during oligodendroglial
 differentiation.";
 RT J. Neurochem. 85:1500-1512(2003).
 RL EMBL; AY185100; AA064470.1; -
 DR SEQUENCE 219 AA; 23720 MW; 30E36041BC1DC66F CRC64;

Query Match 98.9%; Score 996; DB 11; Length 219;
 Best Local Similarity 98.4%; Pred. No. 1.7e-80;

Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGGPRADPLHQMRAGDEFEFRRT 60
 DB 27 MATPASPTDTRALVADFGYKLRQKGYVCGAGPGGPRADPLHQMRAGDEFEFRRT 86
 QY 61 FSDLAQQLHTVTPGSAQQRFTQVSDLFQGGPNWGRVAFVFGALCAESVKNKEPVLVG 120
 DB 87 FSDLAQQLHTVTPGSAQQRFTQVSDLFQGGPNWGRVAFVFGALCAESVKNKEPVLVG 146
 QY 121 QVQEMWVAVLETRLADWIIHSSGGMAEFTALYDGDALBEARRLRSGNMAVRTVLTGAVAL 180
 DB 147 QVQDMWVAVLETRLADWIIHSSGGMAEFTALYDGDALBEARRLRSGNMAVRTVLTGAVAL 206
 QY 181 GALVTGAFPAK 193
 DB 207 GALVTGAFPAK 219

RESULT 3

Q8CGL4 PRELIMINARY; PRT; 193 AA.

AC Q8CGL4;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Bcl2-like protein 2.
 GN BCL2L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Skin;
 RA Su H.-Y.;
 RT "Extraction from neonatal mouse skin after IGF-1 stimulation.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBEP databases.
 DR EMBL; AY170344; AA013177.1; -
 DR MGD; MG1:108052; BCL2.
 DR GO; GO:0016329; P; Apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P; Apoptosis; IEA.
 DR InterPro; IPR000712; BCL2_BH.
 DR InterPro; IPR003093; BCL2_BH.
 DR InterPro; IPR002475; BCL2_FAMILY.
 DR Pfam; PF00452; BCL-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 SQ SEQUENCE 193 AA; 20950 MW; 258AC1816D6FA0 CRC64;

Query Match 94.9%; Score 956; DB 11; Length 193;
 Best Local Similarity 95.3%; Pred. No. 5.1e-77;

Matches 184; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGGPRADPLHQMRAGDEFEFRRT 60
 DB 1 MATPASPTDTRALVAFVGYOLRQKGYVCGAGPGGPRADPLHQMRAGDELQTRFRRT 60
 QY 61 FSDLAQQLHTVTPGSAQQRFTQVSDLFQGGPNWGRVAFVFGALCAESVKNKEPVLVG 120
 DB 61 FSHLAQQLHTVTPGSAQQRFTQVSDLFQGGPNWGRVAFVFGALCAESVKNKEPVLVG 120
 QY 121 QVQEMWVAVLETRLADWIIHSSGGMAEFTALYDGDALBEARRLRSGNMAVRTVLTGAVAL 180
 DB 121 QVQDMWVAVLETRLADWIIHSSGGMAEFTALYDGDALBEARRLRSGNMAVRTVLTGAVAL 180
 QY 181 GALVTGAFPAK 193
 DB 181 GALVTGAFPAK 193

RESULT 4

Q9CYS5 PRELIMINARY; PRT; 178 AA.

AC Q9CYS5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 24, Last annotation update)
 DE Bcl2-like 2.
 GN BCL2L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;

```

RX MEDLINE=2108560; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quakebush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blomstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momaberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
DR EMBL: AK013244; BAB28740.1; -.
DR HSSP: Q07817; 1MA2.
DR MGD: MGI:108052; Bcl2l2.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0006915; F:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match 75.6%; Score 761; DB 11; Length 178;
Best Local Similarity 95.3%; Pred. No. 9.6e-60;
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGBPADPLHQAAPAGDEFEFRFRRT 60
DB 1 MATPASPTDTRALVADFGYKLRQKGYVCGAGPGBPADPLHQAAPAGDEFEFRFRRT 60
QY 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVNKEPELVG 120
DB 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVNKEPELVG 120
QY 121 QVQEMVAVYETRLADWIHSSGGVWVSSQL 150
DB 121 QVQEMVAVYETRLADWIHSSGGVWVSSQL 150

RESULT 5
Q8CER2 PRELIMINARY; PRT; 178 AA.
ID Q8CER2;
AC Q8CER2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bcl2-like 2.
GN BCL2L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;

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RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC040369; AAH40369.1; -.
DR MGD: MGI:108052; Bcl2l2.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0006915; F:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;

Query Match 75.6%; Score 761; DB 11; Length 178;
Best Local Similarity 95.3%; Pred. No. 9.6e-60;
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGBPADPLHQAAPAGDEFEFRFRRT 60
DB 1 MATPASPTDTRALVADFGYKLRQKGYVCGAGPGBPADPLHQAAPAGDEFEFRFRRT 60
QY 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVNKEPELVG 120
DB 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVNKEPELVG 120
QY 121 QVQEMVAVYETRLADWIHSSGGVWVSSQL 150
DB 121 QVQEMVAVYETRLADWIHSSGGVWVSSQL 150

RESULT 6
Q9MTW4 PRELIMINARY; PRT; 233 AA.
ID Q9MTW4;
AC Q9MTW4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bcl-X.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RC Knott J.C., Robertson L., James E.R.;
RA "Rabbit Bcl-X.";
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DE EMBL: AY005131; AAF88137.1; -.
DR HSSP: P53563; IAF3.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0006915; F:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

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Query Match          43.7%; Score 440.5; DB 6; Length 233;
Best Local Similarity 42.0%; Pred. No. 3.8e-31;
Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADFGVGYKLRQKGYC-----GAG-----PGEGRPA 39
DB 6 RELVVDLSTYKLSQGYGWSQPSDVENRTEAPDEGTGEMEPSPAINGNPAMHADSFAV 65
QY 40 D-----PLHQAMRAAGDEFFETFRFTFSDLAQLHVTGSAQQRFTQ 81
DB 66 NCATGSSSLDAREVTPMTAVKQALREAGDEFELRYRPAFSDLSQHLITGTAYQSFQ 125
QY 82 VSDDELFGQGPMMGRVAFVFGAALCAESVKNKEPVLGVQVQEMWVAYLETRLADWTHSS 141
DB 126 VVNELFPRQGVNMGRIVAFSFGALCVESVDKEMEVLSRIAAMWATYLNHLEPWIOEN 185
QY 142 GGMAEFTALYGDGALFEARLRRE--GNMASVRYTLTGAVALGAL 183
DB 186 GGMDFVFLVLYGNNAAESRKQGERPNRFLTGMTVAGVLLGSL 229

RESULT 7
035844 PRELIMINARY; PRT; 233 AA.
AC 035844;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Bcl-xL.
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=Thymus;
RX MEDLINE=98051053; PubMed=9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
apoptosis in T cells."
RL Immunity 7:629-639(1997).
DR EMBL; U51278; AAC53459.1; -.
DR HSSP; P53563; IAF3.
DR MGD; MG186139; Bcl2L.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0016329; F-apoptosis regulator activity; IEA.
DR GO; GO:0006915; P-apoptosis; IEA.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BCL; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;

Query Match          43.2%; Score 435.5; DB 11; Length 233;
Best Local Similarity 41.8%; Pred. No. 1.1e-30;
Matches 94; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 11 RALVADFGVGYKLRQKGYC-----V 28
DB 6 RELVVDLSTYKLSQGYGWSQPSDVENRTEAPDEGTGEMEPSPAINGNPAMHADSFAV 65

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QY 29 CGAGPEGGPAD-----PLHQAMRAAGDEFFETFRFTFSDLAQLHVTGSAQQRFT 80
DB 66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRPAFSDLSQHLITGTAYQSF 124
QY 81 QVSDDELFGQGPMMGRVAFVFGAALCAESVKNKEPVLGVQVQEMWVAYLETRLADWTHS 140
DB 125 QVNELFPRQGVNMGRIVAFSFGALCVESVDKEMQVLVSRIASMWATYLNHLEPWIOE 184
QY 141 SGMAEFTALYGDGALFEARLRRE--JMASVRYTLTGAVALGAL 183
DB 185 NGMDFVFLVLYGNNAAESRKQGERPNRFLTGMTVAGVLLGSL 229

RESULT 8
08SQ42 PRELIMINARY; PRT; 233 AA.
AC 08SQ42;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Bcl-XL protein.
GN BCL-XL.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
RT "Molecular cloning of feline Bcl-2 family "
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080951; BAB85856.2; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0016329; F-apoptosis regulator activity; IEA.
DR GO; GO:0006915; P-apoptosis; IEA.
DR InterPro; IPR007072; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26017 MW; CD17F24F89D47BC9 CRC64;

Query Match          43.0%; Score 433.5; DB 6; Length 233;
Best Local Similarity 41.6%; Pred. No. 1.6e-30;
Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;

QY 11 RALVADFGVGYKLRQKGYC-----V 28
DB 6 RELVVDLSTYKLSQGYGWSRFSQPSDVENRTEAPDEGTGEMEPSPAINGNPAMHADSFAV 65
QY 29 CGAGPEGGPAD-----PLHQAMRAAGDEFFETFRFTFSDLAQLHVTGSAQQRFT 80
DB 66 NGA-TGHSSSLDAREVTPMAAVKQALREAGDEFELRYRPAFSDLSQHLITGTAYQSF 124
QY 81 QVSDDELFGQGPMMGRVAFVFGAALCAESVKNKEPVLGVQVQEMWVAYLETRLADWTHS 140
DB 125 QVNELFPRQGVNMGRIVAFSFGALCVESVDKEMQVLVSRIASMWATYLNHLEPWIOE 184
QY 141 SGMAEFTALYGDGALFEARLRRE--JMASVRYTLTGAVALGAL 193
DB 185 NGMDFVFLVLYGNNAAESRK--GGERSNRFLTGMTVAG-VLLGSLFSRK 233

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RESULT 9
Q9N1A2 PRELIMINARY; PRT; 233 AA.
AC Q9N1A2.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
DE Anti-apoptotic regulator Bcl-XL.
GN BCL-XL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Lee T.L., Ganty J.M.;
RT "PCR Cloning of a Porcine bcl-XL cDNA from Heart.";
RL Submitted (DBS-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216205; AAF33212.1; -.
DR HSSP; Q07817; IMAZ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 42.9%; Score 431.5; DB 6; Length 233;
Best Local Similarity 41.8%; Pred. No. 2,4e-30;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPVGKLRQKGY-----Y 28
DB 6 RELVVDPLSYKLSQKGYWSQFTDVEENRTAEPEGTSEAEPTGSAINGNPSWHLADSPAV 65
QY 29 CGAGPGEGPAPAD-----PLQAMRAAGDEFEFRFRTPSDLAOLHVTGPSAQCRPT 80
DB 66 NGA-TGHSSSLDARREVIAPMAAVKQALREAGDEFELKRRASFSLTQSLHITGTATQSP 124
QY 81 QVSDDELFGGPPNNGRLVAFVFGAALCAESVKNEMEPVGVQVQVMMVAVLETRLADWHS 140
DB 125 QVNVNELFRDGVNMGRIYAFVFGALCVESVDKEMQVLSRIATWATYLNHLBEMWICE 184
QY 141 SGMAEFTALYGDALIEARLRLE--GNMASVTVLTGAVALGAL 183
DB 185 NGGMDTFVELYGNMAAESRKQGERFNRWFLTGMTLAGVLLGSL 229

RESULT 10
Q9MZS7 PRELIMINARY; PRT; 233 AA.
AC Q9MZS7.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
DE Bcl-x long protein.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT "Bcl-x in the sheep ovary.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164517; AAF89532.1; -.
DR HSSP; P53563; IAF3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;

Query Match 42.6%; Score 428.5; DB 6; Length 233;
Best Local Similarity 40.6%; Pred. No. 4,5e-30;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADPVGKLRQKGY-----YCGAGP---GEGPAA 39
DB 6 RELVVDPLSYKLSQKGYWSQFSDVEENRTAEPEGTSDMETGSAINGNPSWHLADSPAV 65
QY 40 D-----PLQAMRAAGDEFEFRFRTPSDLAOLHVTGPSAQCRFTQ 81
DB 66 NGATGHSRLDAREVIAPMAAVKQALREAGDEFELKRRASFSLTQSLHITGTATQSP 125
QY 82 VSDDELFGGPPNNGRLVAFVFGAALCAESVKNEMEPVGVQVQVMMVAVLETRLADWHS 141
DB 126 VNVNELFRDGVNMGRIYAFVFGALCVESVDKEMQVLSRIATWATYLNHLBEMWICE 185
QY 142 GGMAEFTALYGDALIEARLRLE--GNMASVTVLTGAVALGAL 183
DB 186 GGMDTFVELYGNMAAESRKQGERFNRWFLTGMTLAGVLLGSL 229

RESULT 11
Q9BOK4 PRELIMINARY; PRT; 236 AA.
AC Q9BOK4.
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE B-cell leukemia/lymphoma 2.
GN BCL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
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RL Nature 420:563-573 (2002).
DR EMBL: AK049473; BAC33767.1; -.
DR MGD: MGI:88138; Bcl2.
DR GO: GO:0005829; Cytoesol; IDA.
DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR GO: GO:0006915; P:apoptosis; IDA.
DR InterPro: IPR003712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PSS0063; BH4_2; 1.
SQ SEQUENCE 236 AA; 26437 MW; B726BFFA3A1C718 CRC64;

Query Match 41.0%; Score 413; DB 11; Length 236;
Best Local Similarity 37.5%; Pred. No. 1.1e-28;
Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRALVADVFVGYKLRQKGYVCGAG-----PG----- 34
DB 10 DNRREIVMKYIHYLSQRYGEMDADADAPLGAAPFGIFSPESNPFAVRDMART 69
QY 35 -----EGPADP-----LHQAMPAAGDEFETRRFRPSLAQLVHTPSAQQRFTQ 81
DB 70 SPLRLPVATGTPALSPVPVHLLTRAGDDFSRRRRDFAEMSSQLHPTFARGPAT 129
QY 82 VSDELFGQGNMGRLVAFVFGALCAESVKNEMEPLVGVQVEMVAVYETRLADWISS 141
DB 130 VVEELFRDGVNMGRIYAFEFPGVWCVESVNREMSPLVDNIALMTEYLNRHLHTWIDN 189
QY 142 GGNAEFTALYGDGALBEARLRGNMNASVTVLTGVALGALTVCAGAFASK 193
DB 190 GGWDAPVELYG----PSNRPLDFPSWLSLTKTLISLAL-VGACITLIGAVLGKH 236

RESULT 12
Q77SN8 PRELIMINARY; PRT; 236 AA.
ID Q77SN8;
AC Q77SN8;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Bcl2-like protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RT "Rat Bcl2-like protein."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF512835; AAP47159.1; -.
SQ SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;

Query Match 41.0%; Score 413; DB 11; Length 236;
Best Local Similarity 37.5%; Pred. No. 1.1e-28;
Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRALVADVFVGYKLRQKGYVCGAG-----PG----- 34
DB 10 DNRREIVMKYIHYLSQRYGEMDADADAPLGAAPFGIFSPESNPFAVRDMART 69

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QY 35 -----EGPADP-----LHQAMPAAGDEFETRRFRPSLAQLVHTPSAQQRFTQ 81
DB 70 SPLRLPVATGTPALSPVPVHLLTRAGDDFSRRRRDFAEMSSQLHPTFARGPAT 129
QY 82 VSDELFGQGNMGRLVAFVFGALCAESVKNEMEPLVGVQVEMVAVYETRLADWISS 141
DB 130 VVEELFRDGVNMGRIYAFEFPGVWCVESVNREMSPLVDNIALMTEYLNRHLHTWIDN 189
QY 142 GGNAEFTALYGDGALBEARLRGNMNASVTVLTGVALGALTVCAGAFASK 193
DB 190 GGWDAPVELYG----PSNRPLDFPSWLSLTKTLISLAL-VGACITLIGAVLGKH 236

RESULT 13
Q00298 PRELIMINARY; PRT; 238 AA.
ID Q00298;
AC Q00298;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Bcl-XL-like protein 1 (Bcl21 protein).
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX MEDLINE=21239061; PubMed=11406282;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Hsieh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallory S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.R.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF317837; AA81706.1; -.
DR EMBL: BC044130; AA44130.1; -.
DR ZFIN: ZDB-GENE-010730-1; Bcl21.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.

```

DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 SQ SEQUENCE 238 AA; 26253 MW; 6E58394933EEFDB CRC64;

Query Match 40.8%; Score 403; DB 13; Length 238;
 Best Local Similarity 36.6%; Pred. No. 8.4e-28;
 Matches 87; Conservative 27; Mismatches 62; Indels 62; Gaps 6;

QY 11 RALVADPVGYKLRQKGYVC-----GAG----- 32
 DB 6 RELVFFIKYKLSGRNYPCHNIGLTEDNRTDGAENGBGAATLVNCTMRTASS 65
 QY 33 --FEGRPADLPH-----AMRAGDEFETRFRRTSDLAQLHTPGSAQR 78
 DB 66 GTPPQSPASSPQRQTNGSGGLDAVKEALRDSANFEELRYRAFNDSQGHITPATAYG 125
 QY 79 FTQVSDLLFQGGPWWGLVAFVFGALCAESVXKMEPLVGVQVEMVAYLETRLADVI 138
 DB 126 FESVMDVFRDGVWGRIVGLFAGGALCYECVEKEMSPVGRIAEMTVYLDNHIOPMI 185
 QY 139 HSSGMAEFALTALYDGLALEBARLRG--NMA-SVRTVLGVALGALVTGAFPAK 193
 DB 186 QSQGWERFAEIRFKDAASRSKQSFKKMLFAGMTLLTG-----VVGGILIAQK 236

RESULT 14

ID Q7S61 PRELIMINARY; PRT; 79 AA.
 AC Q7S61;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE BCL-WS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=2672518; PubMed=12787069;
 RA Itoh T., Itoh A., Pleasure D.;
 RT "Bcl-2-related protein family gene expression during oligodendroglial
 RT differentiation";
 RU J. Neurochem. 85:1500-1512 (2003).
 DR EMBL; AY185099; AAC64469.1; -
 SQ SEQUENCE 79 AA; 8602 MW; 47EDFB3EE2909485 CRC64;

Query Match 39.8%; Score 402; DB 11; Length 79;
 Best Local Similarity 97.5%; Pred. No. 2.6e-28;
 Matches 77; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 115 MEPLVGQVQEMVAYLETRLADVIHSSGWAFFALTALYDGLAEARLRGNMASVRYTL 174
 DB 1 MEPLVGQVQEMVAYLETRLADVIHSSGWAFFALTALYDGLAEARLRGNMASVRYTL 60
 QY 175 TGAVALGALVTGAFPAK 193
 DB 61 TGAVALGALVTGAFPAK 79

RESULT 15

Q9BDD5 PRELIMINARY; PRT; 180 AA.
 AC Q9BDD5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Anti-apoptotic regulator Bcl-xL (Fragment).
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Amills M., Bouzat J;
 RT "Characterization of the bovine bcl-xL gene and related pseudogenes";
 RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF245488; AAK31307.1; -
 DR EMBL; AF245489; AAK31308.1; -
 DR HSSP; 007817; 1MA2.

DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR00712; BCL2_BH.
 DR InterPro; IPR02475; BCL2_family.
 DR Pfam; PF0452; Bcl-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 180 AA; 20662 MW; 95DC436F95DABDA6 CRC64;

Query Match 39.8%; Score 401; DB 6; Length 180;
 Best Local Similarity 53.5%; Pred. No. 9e-28;
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAGDEFETRFRRTSDLAQLHTVPGSAQRFTQVSDLLFQGGPWWGLVAFVFG 103
 DB 38 QALREAGDEFELRYRARFSDLTSLHTPGTAYGSEGVVNEIFRDGVWGRIVAFSFG 97
 QY 104 AALCAESVXKMEPLVGVQVEMVAYLETRLADVIHSSGWAFFALTALYDGLAEARLR 163
 DB 98 GALCAESVXKMEPLVGVQVEMVAYLETRLADVIHSSGWAFFALTALYDGLAEARLR 157
 QY 164 E--GNMASVRTVLGVALGAL 183
 DB 158 EEFNRWFLTGMTVAGVILGSL 179

Search completed: March 25, 2004, 15:44:26
 Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 15:19:05 ; Search time 10 Seconds
(without alignments)

1004.954 Million cell updates/sec

Title: US-09-155-327G-7

Sequence: 1 MATPASPPTRALVADFGV.....LIGAVAGALVVGAFPSAK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	100.0	193	1	BC1M_HUMAN
2	1000	99.3	193	1	BC1M_MOUSE
3	646.5	64.2	228	1	ARI_XENLA
4	432.5	42.9	229	1	BC1X_CHICK
5	431.5	42.9	233	1	BC1X_PIG
6	428.5	42.6	233	1	BC1X_HUMAN
7	428.5	42.6	233	1	BC1X_MOUSE
8	428.5	42.6	233	1	BC1X_RAT
9	423.5	42.1	233	1	BC1X_CHICK
10	416.5	41.4	229	1	BC1L_BOVIN
11	414	41.1	236	1	BC1L_RAT
12	413	41.0	236	1	BC1L_MOUSE
13	412.5	41.0	239	1	BC1L_HUMAN
14	403	40.0	226	1	BC1L_CHICK
15	371	36.8	204	1	ARI_XENLA
16	177.5	17.6	208	1	BAK_MOUSE
17	176	17.5	211	1	BAK_HUMAN
18	175	17.2	211	1	BAK_HUMAN
19	155.5	15.4	192	1	BAK_MOUSE
20	154.5	15.3	192	1	BAK_MOUSE
21	153	15.2	192	1	BAK_HUMAN
22	150	14.9	280	1	CEB3_MOUSE
23	147	14.6	192	1	BAK_MOUSE
24	146.5	14.5	218	1	BAK_HUMAN
25	143	14.2	177	1	NR13_COTJA
26	137.5	13.7	143	1	BAK_HUMAN
27	136.5	13.6	271	1	CEB3_MOUSE
28	118	11.7	175	1	BC1L_HUMAN
29	117	11.6	194	1	BC1L_HUMAN
30	112	11.1	350	1	WCL1_HUMAN
31	105	10.4	172	1	BC1L_MOUSE
32	99.5	9.9	179	1	EAR_MOUSE
33	98.5	9.8	179	1	EAR_MOUSE

34	98.5	9.8	179	1	EAR_MOUSE	Q07818 african swi
35	87	8.6	3433	1	POLG_KUMTM	P14335 k genome po
36	85.5	8.5	358	1	GINA_LACSA	P23712 lactuca sat
37	85	8.4	275	1	DABP_AGRIS	Q84198 agrobacteri
38	83.5	8.3	660	1	SCQC_BRAVA	P54924 bradyrhizob
39	82.5	8.2	1440	1	POLG_JAEVN	P14403 j genome po
40	82.5	8.2	3432	1	POLG_JAEVN	P13886 j genome po
41	80	7.9	541	1	PRCD_MOUSE	Q91444 m formidido
42	79.5	7.9	872	1	SYA_STREN	Q97448 streptococc
43	79.5	7.9	872	1	SYA_STRE6	Q849C7 streptococc
44	79	7.8	396	1	PORA_PYRFU	Q51804 pyrococcus
45	79	7.8	541	1	PRCD_RAT	O88618 r formidido

ALIGNMENTS

RESULT 1
ID BC1M_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2 (Bcl-2-like 2 protein).
GN BCL2L2 OR BCLM OR KIAA0271.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RT "bcl-2, a novel member of the bcl-2 family, promotes cell survival";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.,
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain";
RL DNA Res. 3:321-329(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RC MEDLINE=22386257; PubMed=12477932;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Mardina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Promotes cell survival.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

```
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL: U59747; AAB09056.1; -.
CC EMBL: D87461; BA19666.1; -.
CC EMBL: BC021198; AAH21198.1; -.
CC HSSP: Q07817; IMAZ.
CC Genew: HGNC:195; BCL2L2.
CC MIM: 601931; -.
CC GO: GO:0008189; F:apoptosis inhibitor activity; TAS.
CC GO: GO:0006916; P:anti-apoptosis; TAS.
CC GO: GO:0007283; P:spermatogenesis; TAS.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR002475; BCL2_family.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC PROSITE: PSS0062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PS00603; BH4_2; 1.
CC KX Apoptosis.
CC FT DOMAIN 9 29 BH4.
CC FT DOMAIN 85 104 BH1.
CC FT DOMAIN 136 151 BH2.
CC SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

Query Match 100.0%; Score 1007; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1,Je-83;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGSPADPLHQARRAGDEFETFRFRT 60
DB 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGSPADPLHQARRAGDEFETFRFRT 60
QY 61 FSDLAQLHVTGSAQQRFTQVSDLEFQGGPMWGLVAFVFGALCAESVNMKEPVLVG 120
DB 61 FSDLAQLHVTGSAQQRFTQVSDLEFQGGPMWGLVAFVFGALCAESVNMKEPVLVG 120
QY 121 QVOEMWVALETRLDWHSISGGMWAFETLVGDGALFEARRLRBNMWSVTVLTGAVAL 180
DB 121 QVOEMWVALETRLDWHSISGGMWAFETLVGDGALFEARRLRBNMWSVTVLTGAVAL 180
QY 181 GALVTGAFPAFASK 193
DB 181 GALVTGAFPAFASK 193
QY 181 GALVTGAFPAFASK 193
DB 181 GALVTGAFPAFASK 193

RESULT 2
BCLM MOUSE STANDARD; PRT; 193 AA.
AC P70345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
```

```
DE Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).
GN BCL2L2 OR BCLW.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.",
RL Oncogene 13:665-675 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/10J; PubMed=9500547;
RA Ross A.U., Maynair K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA Russell L.D., Macgregor G.R.;
RT "Testicular degeneration in Bclw-deficient mice.";
RL Nat. Genet. 18:251-256 (1998).
CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC -----
CC EMBL: U59746; AAB09056.1; -.
CC EMBL: AF030769; AAB86430.1; -.
CC HSSP: Q07817; IMAZ.
CC MGD: MGI:108052; Bcl2l2.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR002475; BCL2_family.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC PROSITE: PSS0062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PSS0063; BH4_2; 1.
CC KX Apoptosis.
CC FT DOMAIN 9 29 BH4.
CC FT DOMAIN 85 104 BH1.
CC FT DOMAIN 136 151 BH2.
CC SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match 99.3%; Score 1000; DB 1; Length 193;
Best Local Similarity 99.0%; Pred. No. 4,7e-83;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGSPADPLHQARRAGDEFETFRFRT 60
DB 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGSPADPLHQARRAGDEFETFRFRT 60
QY 61 FSDLAQLHVTGSAQQRFTQVSDLEFQGGPMWGLVAFVFGALCAESVNMKEPVLVG 120
DB 61 FSDLAQLHVTGSAQQRFTQVSDLEFQGGPMWGLVAFVFGALCAESVNMKEPVLVG 120
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Db 61 FSDLAQIHTPGSAQGRFTQVSDLEFGGPNMGRIVAFFVFGAALCAESVNMKEPLVIG 120
 QY 121 QVQEMWVAYLETRLADWIIHSSGWAFFTAAYGDALBEARRLREGNWSRVTLTGAVL 180
 Db 121 QVQEMWVAYLETRLADWIIHSSGWAFFTAAYGDALBEARRLREGNWSRVTLTGAVL 180
 QY 181 GALVTGAFPAASK 193
 Db 181 GALVTGAFPAASK 193

RESULT 3

ARI_XENLA STANDARD; PRT; 228 AA.

AC 091827;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator R1 (XRI) (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=9531613; PubMed=7607538;
 RA Cruz-Reyes J., Tata J.R.;
 RT "Cloning, characterization and expression of two Xenopus bcl-2-like
 cell-survival genes."
 RL Gene 158:171-179 (1995).
 CC -1- FUNCTION: Could be the homolog of mammalian Bcl-W.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
 CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
 brain of mid-metamorphic to post-metamorphic tadpoles and
 CC adults, where an increase of several fold has been observed.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -----
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 DR EMBL: X82462; CAA57845.1; -
 DR HSSP: Q07817; IMA2;
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; BCL2_family.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02480; Bcl-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS00662; BCL2_FAMILY; 1.
 DR Apoptosis; Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN 120 139 BH1.
 FT DOMAIN 171 186 BH2.
 FT TRANSMEM 207 227 POTENTIAL.
 SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 64.2%; Score 646.5; DB 1; Length 228;
 Best Local Similarity 67.9%; Pred. No. 3,8e-51;
 Matches 125; Conservative 21; Mismatches 35; Indels 3; Gaps 1;
 QY 10 TRALVADFEVGYLROKGYVCGAGPEGPADELHQAMBAAGDEFTRFRFSDLAQLH 69

Db 48 SRALVEDLVRYKLCGRSLV---PEPSGAASCALHAWAAGDEPERROAPSEISTOIH 104
 QY 70 VTPGSAQGRFTQVSDLEFGGPNMGRIVAFFVFGAALCAESVNMKEPLVQVQEMWVAY 129
 Db 105 VTPGTAIVARFAEVAAGSLFPGGVNMGRIVAFVFGAALCAESVNMKEPLPRIQMWVY 164
 QY 130 LETRLADWIIHSSGWAFFTAAYGDALBEARRLREGNWSRVTLTGAVL 189
 Db 165 LETRLADWIIHSSGWAFFTAAYGDALBEARRLREGNWSRVTLTGAVL 224
 QY 190 FASK 193
 Db 225 FASK 228

RESULT 4

BCLX_CHICK STANDARD; PRT; 229 AA.

AC 007816; Q98908;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN BCL2L1 OR BCLX OR BCL-X.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RX MEDLINE=93364977; PubMed=8358789;
 RA Bolise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
 RA Turkula L.A., Mao X., Nunez G., Thompson C.B.;
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
 RT of apoptotic cell death."
 RL Cell 74:597-608 (1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
 RX MEDLINE=97264485; PubMed=9110311;
 RA Villagrosa X., Mezquita C., Mezquita J.;
 RT "Differential expression of bcl-2 and bcl-x during chicken
 RT spermatogenesis."
 RL Mol. Reprod. Dev. 47:26-29 (1997).
 CC -1- FUNCTION: Dominant regulator of apoptotic cell death. The long
 CC isoform promotes cell death repressor activity, whereas the short
 CC isoform promotes apoptosis (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 CC envelope (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=Q07816-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=Q07816-2; Sequence=VSP_000514;
 CC -1- TISSUE SPECIFICITY: Highest expression in organs with lymphoid
 CC development.
 CC -1- FUNCTION: Bcl-X domain seems to be involved in the anti-apoptotic
 CC function. Interacts Bcl1 and Bcl2 domains are required for anti-
 CC apoptotic activity (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -----
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CC -----

DR EMBL; 223110; CAA0657.1; -

DR EMBL; U26645; AAB07677.1; -

DR PIR; A47537; A47537.

DR HSSP; P53563; IAF3.

DR InterPro; IPR000712; Bcl2-BH.

DR InterPro; IPR003093; Bcl2-BH4.

DR InterPro; IPR002475; Bcl2-Family.

DR InterPro; IPR004725; Bcl2-reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRfam; TIGR00865; bcl-2; 1.

DR PROSITE; PSS0062; BCL2_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4; 1; 1.

DR PROSITE; PS0063; BH4_2; 1.

DR Apoptosis; Transmembrane; Alternative splicing.

FT DOMAIN 4 24 BH4.

FT DOMAIN 82 96 BH3.

FT DOMAIN 125 144 BH1.

FT DOMAIN 176 191 BH2.

FT TRANSMEM 206 223 POTENTIAL.

FT VARSPIC 185 229 ERFVLYGNNAAELRKQGFENKMLTGATVAGVLLGLSL
LSRK -> VRTALP (in isoform short).
/FTIDVSP 000514.

SO SEQUENCE 229 AA; 25733 MW; A97D3AD04C059DA CRC64;

Query Match 42.9%; Score 432.5; DB 1; Length 229;
Best Local Similarity 41.7%; Pred. No. 7; 1e-32;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----VCGAGPGGGR----- 37

DB 6 RELVDFVSYKLSQKCHCSELEEDENRTDAEAEMDSVLNGSPSWHPAGHWGAT 65

QY 38 -----AADPLHQAMRAAGDEFEFRFRFTFSDLAQLHTVPGSAQGRFTQVDE 85

DB 66 VARSSLEHETIRASVYRGALPDADDEFELRYRRAFSDLTSGLTTPGTATQSEFQVNE 125

QY 86 LFQGGFNMGRVAFVFGAALCAESVKNEMEPVGVQVQVWVAVYLETRIADWISSGWA 145

DB 126 LFHDGVNMGRIVAFPSFGALCVESVDKEMRYLVGRIVSWMTTYLTDLHDPWIGENGWE 185

QY 146 EFTALYGGALTEBARRLRGNNASVRTVLTGVALGALVTGCAFPASK 193

DB 186 RFVDLYGNNA---AAELRKQGFENKMLTGATVAGVLL-IGSLLSRK 229

RESULT 5

BCLX_PIG STANDARD; PRT; 233 AA.

ID BCLX_PIG 077737;

AC 15-JUL-1999 (rel. 38; Created)

DT 15-JUL-1999 (rel. 38; Last sequence update)

DT 15-MAR-2004 (rel. 43; Last annotation update)

GN Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).

GN BCL2L1 OR BCL2L OR BCLX.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OC NCBI_TaxID=9823;

OX RN (1)

RN SEQUENCE FROM N.A.

RX MEDLINE=99171363; PubMed=10072723;

RA Bartling B., Hoffmann J., Holzer J., Schulz R., Heusch G., Darmer D.;

RT "Quantification of cardioprotective gene expression in porcine short-term hibernating myocardium.";

RL J. Mol. Cell. Cardiol. 33:147-158(1999).

CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-apoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane.

CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to Siva isoform 1 (By similarity).

CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity).

CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death.

CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

CC -1- SIMILARITY: Belongs to the Bcl-2 family.

CC -----

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CC -----

DR EMBL; AJ001203; CAA04597.1; -

DR HSSP; Q07817; IMAZ.

DR InterPro; IPR000712; Bcl2 BH.

DR InterPro; IPR003093; Bcl2-BH4.

DR InterPro; IPR002475; BCL2_Family.

DR InterPro; IPR004725; Bcl2-reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRfam; TIGR00865; Bcl-2; 1.

DR PROSITE; PSS0062; BCL2_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4; 1; 1.

DR PROSITE; PS0063; BH4_2; 1.

DR Apoptosis; Mitochondrion; Transmembrane.

FT DOMAIN 4 24 BH4.

FT DOMAIN 86 100 BH3.

FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.

SO SEQUENCE 233 AA; 26061 MW; 18BF6FA041912B2 CRC64;

Query Match 42.9%; Score 431.5; DB 1; Length 233;
Best Local Similarity 41.8%; Pred. No. 9e-32;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----V 28

DB 6 RELVDFVSYKLSQKCHCSELEEDENRTDAEAEMDSVLNGSPSWHPAGHWGAT 65

QY 29 CGAGPGEGRPAAD-----PLHQAMRAAGDEFEFRFRFTFSDLAQLHTVPGSAQGRFT 80

DB 66 NGA-TGSSSLDAREVTPMAAVQALREAGDEFELRYRRAFSDLTSGLTTPGTATQSEFQVNE 124

QY 81 QVSDDEFQGGFNMGRVAFVFGAALCAESVKNEMEPVGVQVQVWVAVYLETRIADWISS 140

DB 125 QVNLNLFQGGVNMGRVAFPSFGALCVESVDKEMRYLVGRIVSWMTTYLTDLHDPWIGENGWE 184

QY 141 SGMMAEFTALYDGALEBEARLRRE--GNWASVRLTGAVAGAL 183
Db 185 NGGMDTFEYLYGNNAAEBSRKGGRFMRFLTGTLAGVVLISL 229

RESULT 6
BCLX_HUMAN STANDARD; PRT; 233 AA.
AC 007817; O92976;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN BCL2L1 OR BCL2L OR BCLX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.,
RT "bcl-2, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death."
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RA Inohara N., Ohta S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM X(L)).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.S., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP METAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX MEDLINE=95372373; PubMed=764501;
RA Sedlak T.W., Oliva Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA Kornmeyer S.J.;
RT "Multiple Bcl-2 family members demonstrate selective dimerizations
RT with Bax."
RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN [5]
RP METAGENESIS OF BHL AND BH2 DOMAINS.
RX MEDLINE=96170038; PubMed=859636;
RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA Kornmeyer S.J.;
RT "Bax-independent inhibition of apoptosis by Bcl-XL."
RL Nature 379:554-556(1996).
RN [6]
RP INTERACTION WITH SIVA.
RX MEDLINE=22008092; PubMed=12011449;
RA Xue L., Chu F., Cheng Y., Sun X., Borthakur A., Ramazao M., Pandey P.,
RA Mu M., Schlossman S.F., Prasad K.V.S.;
RT "Siva-1 binds to and inhibits Bcl-X(L)-mediated protection against UV
RT radiation-induced apoptosis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:6925-6930(2002).
RN [7]
RP STRUCTURE BY NMR OF 1-209.
RX MEDLINE=97172562; PubMed=9020082;
RA Sattler M., Liang H., Nettelsheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Mittl A.U.,
RA Thompson C.B., Fesik S.W.;
RT "Structure of Bcl-XL-Bak peptide complex: recognition between
RT regulators of apoptosis."
RL Science 275:983-986(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX MEDLINE=96256673; PubMed=8692274;
RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA Yoon H.S., Nettelsheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA Ng S.L., Fesik S.W.;
RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed
RT cell death."
RL Nature 381:335-341(1996).
RN [9]
RP CLEAVAGE BY CASPASES, AND METAGENESIS OF ASP-61.
RX MEDLINE=98118550; PubMed=9435230;
RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
RA Takahashi A., Kaetan M.B., Griffin D.E., Earnshaw W.C., Velluona M.A.,
RA Hardwick J.M.;
RT "Modulation of cell death by Bcl-XL through caspase interaction."
RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
RN [10]
RP FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
RP apoptotic activity is inhibited by association with SIVA isoform
RP 1. Inhibits activation of caspases (By similarity). Appears to
RP regulate cell death by blocking the voltage-dependent anion
RP channel (VDAC) by binding to it and preventing the release of the
RP caspase activator, cytochrome c, from the mitochondrial membrane.
RP The Bcl-X(S) isoform promotes apoptosis.
RP SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2.
RP Heterodimerization with BAX does not seem to be required for anti-
RP apoptotic activity. Isoform Bcl-X(L) binds to SIVA isoform 1.
RP SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
RP envelope (By similarity).
RP ALTERNATIVE PRODUCTS:
RP Event-Alternative splicing; Named isoforms=3;
RP Name=Bcl-X(L); Sequence=Displayed;
RP IsoId=Q07817-1; Sequence=VSP_000515;
RP Name=Bcl-X(S);
RP IsoId=Q07817-2; Sequence=VSP_000515;
RP Name=Bcl-X(beta);
RP IsoId=Q07817-3; Sequence=VSP_000516;
RP TISSUE SPECIFICITY: Bcl-X(S) is expressed at high levels in cells
RP that undergo a high rate of turnover, such as developing
RP lymphocytes. In contrast, Bcl-X(L) is found in tissues containing
RP long-lived postmitotic cells, such as adult brain.
RP DOMAIN: The BH4 domain is required for anti-apoptotic activity.
RP The BH1 and BH2 domains are required for both heterodimerization
RP with other Bcl2 family members and for repression of cell death.
RP PIV: Proteolytically cleaved by caspases during apoptosis. The
RP cleaved protein, lacking the BH4 domain, has pro-apoptotic
RP activity.
RP SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
RP SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
RP SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
RP SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
RP SIMILARITY: Belongs to the Bcl-2 family.
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CC -----
DR EMBL; Z23116; CAAB0663.1; -
DR EMBL; Z23115; CAAB0661.1; -
DR EMBL; U72398; AAB17384.1; -
DR EMBL; BC019307; AAB19307.1; -
DR PIR; B47537; B47537.
DR PIR; JEO203; JEO203.
DR PDB; 1BXU; 29-OCT-97.
DR PDB; 1LXL; 21-APR-97.
DR PDB; 1MAZ; 21-APR-97.
DR PDB; 1G5U; 07-FEB-01.
DR PDB; 1GSM; 21-MAR-01.
DR PDB; 1GJH; 13-JUN-01.
DR Genew; HGNC:992; BCL2L1.
DR MIM; 600839; -.
DR GO; GO:0005739; C:mitochondrion; TAS.
DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0008637; P:apoptotic mitochondrial changes; TAS.
DR GO; GO:0008634; P:negative regulation of survival gene products; TAS.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; P01080; BH1; 1.
DR PROSITE; P01028; BH2; 1.
DR PROSITE; P01259; BH3; 1.
DR PROSITE; P01260; BH4.1; 1.
DR PROSITE; PSS0063; BH4.2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KM 3D-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
FT SITE 61 62 CLEAVAGE (BY CASPASE-1).
FT VARSPLIC 126 188 Missing (in isoform Bcl-X(S)).
FT VARSPLIC 189 233 /Frid=VSP 000515.
FT VARSPLIC 189 233 DTFVELYGNNAABSRKQGERFRNRMFLTMVAGVLLGSL
FT VARSPLIC 189 233 FSRK -> VRTKPLVCPESLAGQSRSPITLLILYFLLCMTI
FT VARSPLIC 189 233 VEDVDS (in isoform Bcl-X(beta)).
FT VARSPLIC 189 233 /Frid=VSP 000516.
FT VARSPLIC 189 233 D->A: NO CLEAVAGE BY CASPASE-1 NOR BY
FT VARSPLIC 189 233 FRD->YRA: NO HETERODIMERIZATION WITH BAX.
FT VARSPLIC 189 233 VNM->ALL: LOSS OF ANTI-APOPTOTIC
FT VARSPLIC 189 233 ACTIVITY.
FT VARSPLIC 189 233 GRI->ELN: LOSS OF ANTI-APOPTOTIC
FT VARSPLIC 189 233 ACTIVITY.
FT VARSPLIC 189 233 G->A: NO HETERODIMERIZATION WITH BAX.
FT VARSPLIC 189 233 G->E: NO HETERODIMERIZATION WITH BAX.
FT VARSPLIC 189 233 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.
FT VARSPLIC 189 233 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.
FT VARSPLIC 189 233 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
FT VARSPLIC 189 233

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CC -----
DR EMBL; Z23116; CAAB0663.1; -
DR EMBL; Z23115; CAAB0661.1; -
DR EMBL; U72398; AAB17384.1; -
DR EMBL; BC019307; AAB19307.1; -
DR PIR; B47537; B47537.
DR PIR; JEO203; JEO203.
DR PDB; 1BXU; 29-OCT-97.
DR PDB; 1LXL; 21-APR-97.
DR PDB; 1MAZ; 21-APR-97.
DR PDB; 1G5U; 07-FEB-01.
DR PDB; 1GSM; 21-MAR-01.
DR PDB; 1GJH; 13-JUN-01.
DR Genew; HGNC:992; BCL2L1.
DR MIM; 600839; -.
DR GO; GO:0005739; C:mitochondrion; TAS.
DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0008637; P:apoptotic mitochondrial changes; TAS.
DR GO; GO:0008634; P:negative regulation of survival gene products; TAS.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; P01080; BH1; 1.
DR PROSITE; P01028; BH2; 1.
DR PROSITE; P01259; BH3; 1.
DR PROSITE; P01260; BH4.1; 1.
DR PROSITE; PSS0063; BH4.2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KM 3D-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
FT SITE 61 62 CLEAVAGE (BY CASPASE-1).
FT VARSPLIC 126 188 Missing (in isoform Bcl-X(S)).
FT VARSPLIC 189 233 /Frid=VSP 000515.
FT VARSPLIC 189 233 DTFVELYGNNAABSRKQGERFRNRMFLTMVAGVLLGSL
FT VARSPLIC 189 233 FSRK -> VRTKPLVCPESLAGQSRSPITLLILYFLLCMTI
FT VARSPLIC 189 233 VEDVDS (in isoform Bcl-X(beta)).
FT VARSPLIC 189 233 /Frid=VSP 000516.
FT VARSPLIC 189 233 D->A: NO CLEAVAGE BY CASPASE-1 NOR BY
FT VARSPLIC 189 233 FRD->YRA: NO HETERODIMERIZATION WITH BAX.
FT VARSPLIC 189 233 VNM->ALL: LOSS OF ANTI-APOPTOTIC
FT VARSPLIC 189 233 ACTIVITY.
FT VARSPLIC 189 233 GRI->ELN: LOSS OF ANTI-APOPTOTIC
FT VARSPLIC 189 233 ACTIVITY.
FT VARSPLIC 189 233 G->A: NO HETERODIMERIZATION WITH BAX.
FT VARSPLIC 189 233 G->E: NO HETERODIMERIZATION WITH BAX.
FT VARSPLIC 189 233 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.
FT VARSPLIC 189 233 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.
FT VARSPLIC 189 233 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
FT VARSPLIC 189 233

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CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope for Bcl-X(L). Cytoplasmic for Bcl-X(delta-TM).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=BCL-X(L);
CC IsoId=Q64373-1; Sequence=Displayed;
CC Name=BCL-X(S);
CC IsoId=Q64373-2; Sequence=VSP_000517;
CC Name=BCL-X(beta);
CC IsoId=Q64373-3; Sequence=VSP_000518;
CC Name=BCL-X(delta-TM);
CC IsoId=Q64373-4; Sequence=VSP_000519;
CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
CC brain, thymus, bone marrow, and kidney. Bcl-X(L) and Bcl-X(delta-
CC TM) expression is enhanced in B and T lymphocytes that have been
CC activated.
CC -1- DEVELOPMENTAL STAGE: Bcl-X(beta) is expressed in both embryonal
CC and postnatal tissues, whereas Bcl-X(L) is predominantly found in
CC postnatal tissues.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC -----
DR EMBL: X83574; CAAS8557.1; -
DR EMBL: L35049; AAA51039.1; -
DR EMBL: L35048; AAA51040.1; -
DR EMBL: U10102; AAA82174.1; -
DR EMBL: U10101; AAA82173.1; -
DR EMBL: U10100; AAA82172.1; -
DR EMBL: U51279; AAC53460.1; -
DR EMBL: U78031; AAB96881.1; -
DR EMBL: U78030; AAB96881.1; JOINED.
DR PIR: I49055; I49055.
DR PIR: I49056; I49056.
DR PIR: I49057; I49057.
DR HSSP: P53563; IAF3.
DR MGD: MGI.88139; Bcl2l.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1; 1.
DR PROSITE: PS01063; BH4_2; 1.
DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.

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FT TRANSMEM 210 226 POTENTIAL.
FT VARSPPLIC 126 188 Missing (in isoform BCL-X(S)).
FT FT /FTId=VSP_000517.
FT VARSPPLIC 189 233 DTFVLYGNNAAESRKGQERFNRFLTGTVAGVILGSL
FT FT FSRK -> VRTFPLVCPPLACVSLCEHP (in isoform
FT BCL-X(beta)).
FT FT /FTId=VSP_000518.
FT VARSPPLIC 194 233 LYGNNAAESRKGQERFNRFLTGTVAGVILGSLFSRK
FT FT -> GHDCGMCSAGLTQSEVTRH (in isoform
FT BCL-X(delta-TM)).
FT FT /FTId=VSP_000519.
SQ SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CRC64;
Query Match 42.6%; Score 428.5; DB 1; Length 233;
Best Local Similarity 41.3%; Pred. No. 1.7e-31;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;
QY 11 PALVDFYGYKLRQGY-----Y 28
Db 6 RELVDFLSTKLQCKYWSQPSVDENRTEAPETEARTEPSAINGPSWHLADSPAV 65
QY 29 CGAGPGEQPAD-----PLHQMRAGDEPFRFRPTPSDIAOLHTVPGSAQGRFT 80
Db 66 NGA-TGHSSSIDAREVTPMAVKQALRAGDEPFLRYRARSDDLTSQHLTPGAYGSE 124
QY 81 QVSDLEFGCGNNGRLVAFVFGAALCAESYKMEPLVGVQCEMVAVYETRLADWTHS 140
Db 125 QVNNLEFPGDGVNMGRTVAFSFGGALCVESYDKEMQVLSRIASMMATYINDHLEPPIQ 184
QY 141 SGNAEPFALYDGDALREARLR--GNWASVRVTLGAVAGL 183
Db 185 NGMDTFVDLYGNNAAESRKGQERFNRFLTGTVAGVILGSL 229
RESULT 8
BCLX_RAT STANDARD, PRT, 233 AA.
AC P53563; P70613; P70614; Q62678; Q62836; Q64087; Q64128;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN BCL2L1 OR BCL2L OR BCLX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC TISSUE=Brain;
RA Michaelidis T.M.;
RU Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Wesselingh S.L.; David G.L.; Choi S.; Veliuona M.; Hardwick J.M.;
RU Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC TISSUE=Thymus;
RA MEDLINE=96278736; PubMed=8662675;
RA Saitawa N.; Inohara N.; Okada S.; Yuzaki M.; Shoji S.-I.; Ohta S.;
RT "An additional form of rat Bcl-X, Bcl-xbeta, generated by an
RT unspliced RNA, promotes apoptosis in promyeloid cells."
RL J. Biol. Chem. 271:13258-13265(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=55128487; PubMed=7828536;
RA Tilly J.L.; Tilly K.L.; Kenton M.L.; Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive

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RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 RN [5]
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RA MEDLINE=96010630; Pubmed=9346936;
 RA Morikawa K., Kunishima N., Inohara N., Ishbaashi Y., Ohta S.,
 RT "Crystal structure of rat Bcl-XL. Implications for the function of
 the Bcl-2 protein family";
 RL J. Biol. Chem. 272:27886-27892(1997).
 CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
 apoptotic activity is inhibited by association with SIVA isoform
 1. Inhibits activation of caspases (By similarity). Appears to
 regulate cell death by blocking the voltage-dependent anion
 channel (VDAC) by binding to it and preventing the release of the
 caspase activator, cytochrome c, from the mitochondrial membrane.
 CC The Bcl-X(S) and Bcl-X(beta) isoforms promote apoptosis.
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
 similarity). Heterodimerization with BAX does not seem to be
 required for anti-apoptotic activity (By similarity). Isoform Bcl-
 X(L) binds to Siva isoform 1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 envelope (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=Bcl-X(L);
 CC IsoId=P53563-1; Sequence=displayed;
 CC Name=Bcl-X(S);
 CC IsoId=P53563-2; Sequence=VSP_000520;
 CC Name=Bcl-X(beta);
 CC IsoId=P53563-3; Sequence=VSP_000521;
 CC -1- TISSUE SPECIFICITY: Expressed in most tissues. Bcl-X(beta) is
 specifically expressed in cerebellum, heart, and thymus. In the
 ovary, the predominant form is Bcl-X(L), with a small but
 detectable level of Bcl-X(S).
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
 CC The BH1 and BH2 domains are required for both heterodimerization
 with other Bcl2 family members and for repression of cell death.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 cleaved protein, lacking the BH4 domain, has pro-apoptotic
 activity (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X82537; CAAS7886.1; -
 CC EMBL: X82537; CAAS7887.1; -
 CC EMBL: U10579; AAA19257.1; -
 CC EMBL: U72350; AAB17353.1; -
 CC EMBL: U72348; AAB17352.1; -
 CC EMBL: U34963; AAA77686.1; -
 CC EMBL: S76513; AAC60701.2; ALT_INIT.
 CC EMBL: S78284; AAC60702.1; -
 CC PIR: I67431; I67431.
 CC PIR: S51761; S51761.
 CC PDB: 1AE3; 07-JUL-97.
 CC InterPro: IPR000712; Bcl2_BH.
 CC InterPro: IPR003093; Bcl2_BH4.
 CC InterPro: IPR002475; Bcl2_family.
 CC InterPro: IPR004725; Bcl2_reg.
 CC Pfam: PF00452; Bcl-2; 1.
 CC Pfam: PF02180; BH4; 1.
 CC SMART: SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KM Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
 3D-structure.
 FT DOMAIN 4 24
 FT DOMAIN 86 100 BH4.
 FT DOMAIN 129 148 BH3.
 FT DOMAIN 180 195 BH1.
 FT TRANSMEM 210 226 BH2.
 FT TRANSMEM 126 188 POTENTIAL.
 FT VASAPLIC 189 233 Missing (in isoform Bcl-X(S)).
 FT VASAPLIC 189 233 /FtId=VSP_000520.
 FT VASAPLIC 189 233 DTFVLYGNNAASRSRQGRFNRFLTGAVVLLGSL
 FT VASAPLIC 189 233 PSRK -> VRTTPLYCPCLTCLSVETPNCQFPMRGVVED
 FT VASAPLIC 189 233 IDYSGDIPGL (in isoform Bcl-X(beta)).
 FT VASAPLIC 189 233 /FtId=VSP_000521.
 FT VASAPLIC 189 233 R -> Q (IN REF. 1).
 FT VASAPLIC 189 233 F -> S (IN REF. 2).
 FT VASAPLIC 189 233 A -> E (IN REF. 2).
 FT VASAPLIC 189 233 I -> L (IN REF. 4).
 FT VASAPLIC 189 233 A -> V (IN REF. 4).
 FT VASAPLIC 189 233 FF -> SS (IN REF. 4).
 FT VASAPLIC 189 233 A -> T (IN REF. 4).
 FT VASAPLIC 189 233 A -> P (IN REF. 4).
 FT TURK 20 21
 FT TURK 25 28
 FT TURK 82 83
 FT HELIX 84 100
 FT HELIX 106 112
 FT TURK 116 117
 FT HELIX 120 127
 FT HELIX 128 131
 FT TURK 132 133
 FT HELIX 137 156
 FT TURK 157 158
 FT TURK 160 161
 FT HELIX 162 177
 FT TURK 178 178
 FT HELIX 179 184
 FT TURK 185 186
 FT HELIX 187 195
 SQ SEQUENCE 233 AA; 26158 MW; 2B62B6C3864BC8F CRC64;
 Query Match 42.6%; Score 428.5; DB 1; Length 233;
 Best Local Similarity 41.3%; Pred. No. 1,7e-31;
 Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPVGKLRQGY-----V 28
 Db 6 RELVVDLISYKLSQGYSMGQFSDEENRTAEDETEPERETPSAINGNPSMLADSPAV 65
 QY 29 CGAGPGEGRPAD-----PLIQARAGDDEETFRFRFSLLAQHTPPSAQORFT 80
 Db 66 NGA-TGHSSTSLDAREVIMPAVQALREAGDEBELYRRAFSDLTQSLHTTPTAYQSFE 124
 QY 81 QVSDPEFOGGPNNGRLVAFVFGAALCAEENVNEMPELVQGVQGVNVAVYETSLADMIHS 140
 Db 125 QVNNELFRDGVNNGRIYAFSPGALCYESVDKEMOVLVSRIASNNATYINDHLEFRIOE 184
 QY 141 SGGVAEFTALYGDGALAEARLRE--GNVASYRTVLTGAVALGAL 183
 Db 185 NGGWDTFVDLYGNNAASRSRQGRFNRFLTGAVVLLGSL 229
 RESULT 9
 BCL2_CHICK STANDARD; PRT; 233 AA.
 ID BCL2_CHICK

AC 000709;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2
 OS Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RX MEDLINE=92375724; PubMed=1508712;
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
 RT "Isolation and characterization of the chicken bcl-2 gene: expression
 in a variety of tissues including lymphoid and neuronal organs in
 adult and embryo.";
 RL Nucleic Acids Res. 20:4187-4192(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell lymphoma;
 RX MEDLINE=92379084; PubMed=1511008;
 RA Casalis-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
 homologue of the Bcl-2 oncoprotein";
 RL Biochim. Biophys. Acta 1132:109-113(1992).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
 CC kidney, heart, ovary and brain, with the highest levels in the
 CC thymus. In the embryo, highly levels expressed in all tissues with
 CC high levels in the bursa of Fabricius.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAIF-1 (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -----
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 CC -----
 DR EMBL; D13382; BAA01978.1; -;
 DR EMBL; D13381; BAA01978.1; JOINED.
 DR EMBL; Z11961; CAA78018.1; -;
 DR PIR; A37332; A37332.
 DR PIR; S24390; S24390.
 DR HSSP; Q07817; 1MAZ.
 DR InterPro; IPR000712; Bcl2.BH.
 DR InterPro; IPR003093; Bcl2.BH.
 DR InterPro; IPR002475; Bcl2 family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF00452; Bcl-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.
 DR TIGR; TIGR00865; bcl-2; 1.
 DR PROSITE; PS00682; BCL2 FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS00683; BH4-2; 1.
 KM Apoptosis; Transmembrane; Mitochondrion.
 FT DOMAIN 10 30 BH4.
 FT DOMAIN 87 101 BH3.
 FT DOMAIN 130 149 BH1.
 FT DOMAIN 181 196 BH2.
 FT TRANSMEM 208 228 POTENTIAL.
 FT CONFLICT 64 64 E -> S (IN REF. 2).
 FT CONFLICT 67 82 GSAAAEVPPAPGLRP -> ARLLVRCPRRLGCA
 (IN REF. 2).
 FT CONFLICT 121 121 H -> T (IN REF. 2).
 FT CONFLICT 139 139 G -> V (IN REF. 2).
 SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6E4C3D CRC64;
 Query Match 42.1%; Score 423.5; DB 1; Length 233;
 Best Local Similarity 38.0%; Pred. No. 4; 7e-31;
 Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;
 QY 9 DTRALVADPVGKLRKQGYVCGAG-----PGSGPADP----- 41
 DB 10 DNRKELVKIHYKLSQRGDWAAGEDRPVPPAPAPAAVAAGAASHRRFPESA 69
 QY 42 -----LHQMRAAGDEFFRRFRRTSDLAQLHTVGSAGQPRQVSD 84
 DB 70 AASEVPAPGLRPAPGGVHALRQGDFFSRYPQDFQMGQLHTFTAGRGVAVE 129
 QY 85 ELFGGPPMGRILVAFVFGALCASVKEPELVGVQVEMVYLETRLDMTHSSGGM 144
 DB 130 ELFRGVGVAGRIVAFFEGGVCVCSVVRMSPLVDNIAITMTETLNRHLNMIQDNGM 189
 QY 145 AFTALYDGALEEARLRLEGNMASVRLTGAVALGALVTGAFPAASK 193
 DB 190 DAFVELYGN----SWRPPLFDRSWISLKITLS-LVLVGACITLGAIVLGHK 233
 RESULT 10
 BCL2 BOVIN
 ID BCL2 BOVIN STANDARD; PRT; 229 AA.
 AC 002718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein; TISSUE=Thymus;
 RX MEDLINE=98162580; PubMed=9501056;
 RA Reyes R.A., Cockrell G.L.;
 RT "Increased virus of bcl-2/bax expression is associated with bovine
 RT leukemia virus-induced leukemogenesis in cattle".
 RL Virology 242:184-192(1998).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1) (By similarity).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2

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CC domains, and is necessary for anti-apoptotic activity. Also
CC interacts with APAF-1, RAF-1 and p53BP2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum (By
CC similarity).
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated
CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
CC similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity (By similarity).
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U92434; AAB53319.1; -
CC HSSP: Q07817; 1MAZ.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR002475; BCL2_family.
CC InterPro: IPR004725; Bcl2_reg.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC TIGRFAMs: TIGR00865; bcl-2; 1.
CC PROSITE: PS50062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01259; BH3; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PS50063; BH4_2; 1.
CC Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
CC FT DOMAIN 10 30 BH4.
CC FT DOMAIN 64 68 POLY-PRO.
CC FT DOMAIN 69 72 POLY-ALA.
CC FT DOMAIN 83 97 BH3.
CC FT DOMAIN 126 145 BH1.
CC FT DOMAIN 177 192 BH2.
CC TRANSMEM 202 223 POTENTIAL.
CC SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
CC MOD RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
CC SEQUENCE 229 AA; 25099 MW; ADIDDAF98FFIIDD CRG64;
Query Match 41.4%; Score 416.5; DB 1; Length 229;
Best Local Similarity 38.2%; Pred. No. 2e-30;
Matches 86; Conservative 35; Mismatches 59; Indels 45; Gaps 5;
QY 9 DRRALVADVGVYLRKXGVYCGAG-----PGS----- 35
DB 10 DNRRIYWKRIHYLTSRGYEMDAGDGAAPPGAAPAGILSSQPGSTPAPSTSPPPPA 69
36 ---GPAADP---LHOAPRAAGDEFETRRRTFSDLAALHTVPGSAGQRFQVSDDELFG 88
DB 70 AAAGPAPSPVPPVHLTLRAGDDFRRIRRDPAEMSSQLHTLPTARERFATVVEELFR 129

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QY 89 GGNWGRILVAFVEGALCAESVKNENPLVGQVQEMWVAYLETRLADMTSSGGMAEFT 148
DB 130 DGNVWGVIVAFBERGGVWCVESVNRKMSPLVDSIALWMTXYLNRHHTWTLQDNGWDFAV 169
QY 149 ALYEDGALIEERKRLRDEGNWASVRTVLTGAVALGALVTVGAFPPASK 193
DB 190 ELYG----PSMRPFPDPSWLSLKALSLAL-VGACITLGAVALGRK 229
RESULT 11
BCL2_RAT STANDARD; RAT; 236 AA.
AC P49950; Q62837; Q64032;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2 OR BCL-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94193015; PubMed=8144041;
RA Sato T., Irie S., Krajewski S., Reed J.C.;
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL Gene 140:291-292(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=95129487; PubMed=7828536;
RA Tilly U.L., Tilly K.L., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-x long messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
RN [3]
RP SEQUENCE OF 19-172 FROM N.A.
RX MEDLINE=95059917; PubMed=7969891;
RA Castren B., Ohga Y., Berzaghi M.P., Tzimasiorgis G., Thoenen H.,
RA Lindholm D.;
RT "bcl-2 messenger RNA is localized in neurons of the developing and
RT adult rat brain.";
RL Neuroscience 61:165-177(1994).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity. Also
CC interacts with APAF-1, RAF-1 and p53BP2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
CC highest levels in reproductive tissues. In the adult brain,
CC expression is localized in mitral cells of the olfactory bulb,
CC granule and pyramidal neurons of hippocampus, pontine nuclei,
CC cerebellar granule neurons, and in ependymal cells. In prenatal
CC brain, expression is higher and localized in the neuroepithelium
CC and in the cortical plate.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and

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occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatase 2A (PP2A) (by similarity).

- P1M: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

- SIMILARITY: Belongs to the Bcl-2 family.

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DR EMBL: U14680; AA03662.1; -

DR EMBL: U14964; AA07687.1; -

DR EMBL: S74122; -; NOT_ANNOTATED_CDS.

DR PIR: 153744; 153744.

DR PIR: 167432; 167432.

DR HSSP: Q07817; 1MA2.

DR InterPro: IPR000712; Bcl2_BH.

DR InterPro: IPR003093; Bcl2_BH4.

DR InterPro: IPR002475; Bcl2_family.

DR InterPro: IPR004725; Bcl2_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BH4; 1.

DR SMART: SM00265; BCL; 1.

DR TIGRfams: TIGR00865; bcl-2; 1.

DR PROSITE: PS00662; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4_1; 1.

DR PROSITE: PS00063; BH4_2; 1.

DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.

FT DOMAIN 10 30 BH4.

FT DOMAIN 90 104 BH3.

FT DOMAIN 133 152 BH1.

FT DOMAIN 184 199 BH2.

FT TRANSMEM 209 230 POTENTIAL.

FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

FT MOD_RES 70 75 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

FT CONFLICT 42 42 A -> R (IN REF. 2).

FT CONFLICT 157 157 S -> G (IN REF. 1).

FT CONFLICT 164 164 S -> Y (IN REF. 2).

FT CONFLICT 212 212 L -> Q (IN REF. 2).

FT SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;

SC

Query March 41.1%; Score 414; DB 1; Length 236;

Best Local Similarity 36.2%; Pred. No. 3,4e-30;

Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

CC 142 GGNWAEFTALYDGCALFEARLRKGNWASRYTLTGVALGALVWGAFPSK 193

CC |||||

CC Db 190 GGNDAFEVLYG-----PSMPLDPFSLSTKLSTLAL-VGACITTGAYGHK 236

CC

CC RESULT 12

CC BCL2_MOUSE

CC ID BCL2_MOUSE STANDARD; PRT; 236 AA.

CC AC P10417; P10418; 10; Created)

CC DT 01-MAR-1989 (Rel. 10; Last sequence update)

CC DT 01-APR-1993 (Rel. 25; Last sequence update)

CC DT 15-MAR-2004 (Rel. 43; Last annotation update)

CC DE Apoptosis regulator Bcl-2.

CC GN BCL2 OR BCL-2.

CC OS Mus musculus (Mouse).

CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

CC OX NCBI_TaxID=10090;

CC RN [1]

CC RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).

CC RC STRAIN=BALB/c; TISSUE=Liver;

CC RX MEDLINE=87187643; PubMed=3032455;

CC RA Negishi M., Silit F., Kozak C., Tsujimoto Y., Croce C.M.;

CC RT "Molecular analysis of bcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";

CC RL Cell 49:455-463 (1987).

CC RN [2]

CC RP REVISIONS TO 221-222.

CC RX MEDLINE=92375724; PubMed=1508712;

CC RA Eguchi Y., Ewert D.L., Tsujimoto Y.;

CC RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";

CC RL Nucleic Acids Res. 20:4187-4192 (1992).

CC RN [3]

CC RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.

CC RX MEDLINE=9727291; PubMed=9115213;

CC RA Ito T., Deng X., Carr B., May W.S., Jr.;

CC RL "Bcl-2 phosphorylation required for anti-apoptosis function.";

CC RN J. Biol. Chem. 272:11671-11673 (1997).

CC RN [4]

CC RP DEPHOSPHORYLATION BY PP2A.

CC RX MEDLINE=99069407; PubMed=9852076;

CC RA Deng X., Ito T., Carr B., Mumby M., May W.S., Jr.;

CC RT "Reversible phosphorylation of Bcl2 following interleukin 3 or bryostatine 1 is mediated by direct interaction with protein phosphatase 2A.";

CC RL J. Biol. Chem. 273:34157-34163 (1998).

CC CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (Apaf-1).

CC CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Interacts with TP53BP2 (By similarity). Also interacts with APAF-1 and RAIF-1.

CC CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

CC CC -1- ALTERNATIVE PRODUCTS:

CC CC Event=Alternative splicing; Named isoforms=2;

CC CC Name=Alpha;

CC CC IsoId=P10417-1; Sequence=Displayed;

CC CC Name=Beta;

CC CC IsoId=P10417-2; Sequence=VSP_000513;

CC CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.

CC CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAIF-1.

CC CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation

on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A).
CC - PPM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.
CC - SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC - SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC - SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC - SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC - SIMILARITY: Belongs to the Bcl-2 family.

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CC
CC EMBL: L31532; AAA37282.1; -
CC EMBL: M16506; AAA37282.1; JOINED.
CC EMBL: M16506; AAA37281.1; -
CC PIR: B25960; TVMSB1.
CC HSSP: Q07817; IMAZ.
CC MGD: MGI:88138; Bcl2.
CC DR GO: GO:0005829; Cytosol; IDA.
CC DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.
CC DR GO: GO:0005515; F:protein binding; IPI.
CC DR InterPro: IPR00712; Bcl2 BH.
CC DR InterPro: IPR003093; Bcl2 BH.
CC DR InterPro: IPR002475; Bcl2 family.
CC DR InterPro: IPR004725; Bcl2_reg.
CC DR Pfam: PF00452; Bcl-2; 1.
CC DR Pfam: PF0180; BH4; 1.
CC DR SMART: SMO0337; BCL; 1.
CC DR SMART: SMO0265; BH4; 1.
CC DR TIGRfam: TIGR00865; bcl-2; 1.
CC DR PROSITE: PS00562; BCL2_FAMILY; 1.
CC DR PROSITE: PS01080; BH1; 1.
CC DR PROSITE: PS01258; BH2; 1.
CC DR PROSITE: PS01259; BH3; 1.
CC DR PROSITE: PS01260; BH4; 1.
CC DR PROSITE: PS00653; BH4_2; 1.
CC DR Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; KW Phosphorylation.
CC FT DOMAIN 10 30 BH4.
CC FT DOMAIN 90 104 BH3.
CC FT DOMAIN 133 152 BH1.
CC FT DOMAIN 184 199 BH2.
CC FT TRANSMEM 209 230 POTENTIAL.
CC FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
CC FT MOD RES 70 70 PHOSPHORYLATION (BY PKC).
CC FT VARSLIC 193 236 DAFVEIYGRSMRPLPFPSSFKITLSALVACTITLNAVIL
GRK -> VQACIVE (in isoform Beta).
FT FT
SQ SEQUENCE 236 AA; 26425 MW; AAB5EF6B0766B0A CRC64; /FTID=VSP 000513.
Query Match 41.0%; Score 413; DB 1; Length 236;
Best Local Similarity 37.5%; Pred. No. 4.2e-30;
Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;
QY 9 DTFALVADVGVYLRKQGYVCGAG-----PG----- 34
DB 10 DNRREIMWKIHYKLSRGVEMDADADAPLGAAPFPGFSPQPSNPMVAHREMAART 69
QY 35 -----EGPADP-----LHOAMKAGDEDEFTRFRRTSLAQLAHLVTPGSAQGRFTQ 81
DB 70 SPURPVATAGPALSPVPCVHLTLRRAGDDFSRRYRDRFAMSSQHLPTTAGRPAT 129

QY 82 VSDLEFQCGNMGVLVAFVFGAALCAESYKNEKEDLVGOQEMVAYLETSLADWTHSS 141
DB 130 VVEELFRQGVNMGRIIVAFEFEGVWCVESVREMSPLVDNIALMTETLYLNRLHATWIGDN 189
QY 142 GGMDEFTALVYDGLALBEARLRREGNMASVPTVLTGVAALGALVYVAFPSK 193
DB 190 GGMDFVVELYV-----PSMRPLPFPSSFKITLSAL-VGACITLGAIVLGRK 236
RESULT 13
BCL2_HUMAN
ID BCL2_HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q13842; Q16197;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Ebnuchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Grantinger W., Bennett S.;
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation of the bcl-2-ig fusion gene in lymphoma.";
RL EMBO J. 7:123-131(1988).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARIANT THR-43.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Foel C.L., Robertson P.D., Schachwitz W.S., Sherwood J.K., Wiltrik L.A., Nickerson D.A.;
RN Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RP [6]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dlatcenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stempelen M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Rata S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mallary S.J., Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RN SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS
RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILE-93.
RX MEDLINE=92096610; PubMed=1339299;
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.,
RT "Frequent incidence of somatic mutations in translocated BCL2
RT oncogenes of non-Hodgkin's lymphomas.";
RL Blood 79:229-237(1992).
RN [8]
RN SUBCELLULAR LOCATION.
RP MEDLINE=91066924; PubMed=2250705;
RX Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.,
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT programmed cell death.";
RL Nature 348:334-336(1990).
RN [9]
RN MUTAGENESIS.
RX MEDLINE=94239528; PubMed=8183370;
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.,
RT "BHL and BH2 domains of Bcl-2 are required for inhibition of
RT apoptosis and heterodimerization with Bax.";
RL Nature 369:321-323(1994).
RN [10]
RN CLEAVAGE BY CASPASES, AND MUTAGENESIS.
RX MEDLINE=98057466; PubMed=9395403;
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kasran M.B., Bedi A.,
RA Ueno K., Hardwick J.M.,
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
RL Science 278:1966-1968(1997).
RN [11]
RN INTERACTION WITH TP53BP2.
RX MEDLINE=96251339; PubMed=8668206;
RA Naumovski L., Cleary M.L.,
RT "The p53-binding protein 53BP2 also interacts with Bcl2 and impedes
RT cell cycle progression at G2/M.";
RL Mol. Cell. Biol. 16:3884-3892(1996).
RN [12]
RN REVIEW ON PHOSPHORYLATION.
RX MEDLINE=21260650; PubMed=11368354;
RA Ruvoilo P.P., Deng X., May W.S.,
RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
RL Leukemia 15:515-522(2001).
RN [13]
RN PHOSPHORYLATION BY ASK1/JNK1.
RX MEDLINE=20036804; PubMed=10567572;
RA Yamamoto K., Ichijo H., Korsmeyer S.J.,
RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
RT protein kinase pathway normally activated at G(2)/M.";
RL Mol. Cell. Biol. 19:8469-8478(1999).
RN [14]
RN FUNCTION: Suppresses apoptosis in a variety of cell systems
RN including factor-dependent lymphohematopoietic and neural cells.
RN Regulates cell death by controlling the mitochondrial membrane
RN permeability. Appears to function in a feedback loop system with
RN caspases. Inhibits caspase activity either by preventing the
RN release of cytochrome c from the mitochondria and/or by binding to
RN the apoptosis-activating factor (APAF-1).
RN SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
RN Bcl-X(L). Heterodimerization with BAX requires intact BHL and BH2
RN domains, and is necessary for anti-apoptotic activity (By
RN similarity). Also interacts with APAF-1, Raf-1 and TP53BP2.
RN SUBCELLULAR LOCATION: Outer mitochondrial membrane, intercellular
RN membrane of the nuclear envelope and the endoplasmic reticulum.

CC -1- ALTERNATIVE PRODUCTS;
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=PI0415-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=PI0415-2; Sequence=VSP_000512;
CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with Raf-1.
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type
CC II chronic lymphatic leukemia) by a chromosomal translocation
CC t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene
CC regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying
CC the chromosomal translocation could be attributed to the Ig
CC somatic hypermutation mechanism resulting in nucleotide
CC transitions.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BCL2ID49.html".
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL, M13994; AAA51813.1; ALT_SEQ.
CC EMBL, M13995; AAA51814.1; ALT_SEQ.
CC EMBL, M14745; AAA35581.1;
CC EMBL, X06467; CAA29778.1; -.
CC EMBL, AY220759; AAO26045.1; -.
CC EMBL, BC027258; AAH27258.1; -.
CC EMBL, S72602; AAD14111.1; ALT_SEQ.
CC PIR, B29409; TVHIB1.
CC PIR, C37332; TVHIB1.
CC PDB, 1G5W; 2I-JUN-01.
CC PDB, 1G7H; 13-JUN-01.
CC Genew; HGNC:990; BCL2.
CC MIM: 151430; -.
CC GO, GO:0005743; C:mitochondrial inner membrane; TAS.
CC GO, GO:0008189; F:apoptosis inhibitor activity; TAS.
CC GO, GO:0006916; P:anti-apoptosis; TAS.
CC GO, GO:0006959; P:humoral immune response; TAS.
CC GO, GO:0008285; P:negative regulation of cell proliferation; TAS.
CC GO, GO:0000074; P:regulation of cell cycle; TAS.
CC InterPro, IPR00712; Bcl2_BH.
CC InterPro, IPR003093; Bcl2_BH4.
CC InterPro, IPR02475; Bcl2_family.
CC InterPro, IPR004725; Bcl2_reg.
CC
CC Query Match 41.0%; Score 412.5; DB 1; Length 239;
CC Best Local Similarity 37.0%; Pred. No. 4.7e-30;
CC Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;
CC 9 DTRALVADFVGKXKROKGYVCGAG-----PGE----- 35


```

Db      10 DNEIIVKVIHYKLSQRYGWDAGVGAAPGAAPAGIFSSQPGHTPPAASRDVART 69
Qy      36 -----GPAADP-----LHQAMRAGDEFEFRFRFRFSQDLAQLHTPSQAQR 78
Db      70 SPLQTPAAGAAAGPALSPVPVAVHLLTKQAGDFFRRYRDRDAEMSSQLHTLPTAR 129
Qy      79 FTQVSDLEFGGPNMRLVAFVFGAALCAESYKEMEPVQGVQVQVMMVAYLETRLADWI 138
Db      130 FAVVBELEFRDGVNWKIRIVAFEFEGVWCVESYRMSPLVNDIALMTEYINRLHWTI 189
Qy      139 HSGGMAEFTALYGDGALBEARLRGNASVRTVITGAVALGALTVGAFFASK 193
Db      190 QDNGWDAPFVELYX----PSMRPLFPDSWLSKTLISLAL-VGACITLIGYLGKH 239

RESULT 14
BCL2_CR1LO STANDARD; PRT; 236 AA.
AC 09JYB8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary; PubMed=10973819;
RA MEDLINE=20431763;
RX Tomicic M.T., Christmann M., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RT protein.";
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=11181062;
RA Tomicic M.T., Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT and caspase-3.";
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including caspase-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity. Also
CC interacts with APAF-1, RAF-1 and TP53BP2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated kinases
CC (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC (By similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

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CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AJ271720; CAB92245.1; -.
DR PIR; J07383; J07383.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01256; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN 10
FT DOMAIN 30
FT DOMAIN 90
FT DOMAIN 104
FT DOMAIN 133
FT DOMAIN 152
FT DOMAIN 184
FT DOMAIN 199
FT TRANSMEM 209
FT SITE 64
FT SITE 65
FT MOD_RES 70
FT SEQUENCE 236 AA; 26491 MW; BECADFLIEF337228 CRC64;

Query Match 40.0%; Score 403; DB 1; Length 236;
Best local similarity 35.3%; Pred. No. 3.4e-29;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;

Qy 9 DTRALVADFGYKLRQKY----- 27
Db 10 DNEIIVKVIHYKLSQRYGWDAGVGAAPGAAPAGIFSSQPGHTPPAASRDVART 69
Qy 28 -----VCGAGPGEPAADPLHQAMRAGDEFEFRFRFRFSQDLAQLHTPSQAQRFTQ 81
Db 70 SPLRPIVATGPTLSPVPVAVHLLTKRAGDFFRRYRDRDAEMSSQLHTLPTAR 129
Qy 82 VSDLEFGGPNMRLVAFVFGAALCAESYKEMEPVQGVQVQVMMVAYLETRLADWIHSS 141
Db 130 FAVVBELEFRDGVNWKIRIVAFEFEGVWCVESYRMSPLVNDIALMTEYINRLHWTIQDN 189
Qy 142 GGMAEFTALYGDGALBEARLRGNASVRTVITGAVALGALTVGAFFASK 193
Db 190 QDNGWDAPFVELYX----PSMRPLFPDSWLSKTLISLAL-VGACITLIGYLGKH 236

RESULT 15
AR11_XENLA STANDARD; PRT; 204 AA.
AC 091828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2 (Xenopus).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.

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OK NCBI_TaxID=8355;
RN [1]
RF SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=9531613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell-survival genes.";
RL Gene 158:171-179(1995).
CC -1- FUNCTION: Confers strong protection against cell death.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC brain of mid-metamorphic to post-metamorphic tadpoles and
CC adults, where an increase of several fold has been observed.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC -----
DR EMBL; X82461; CA57844.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRfam; TIGR00865; bcl-2; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT DOMAIN 101..120 BH1.
FT DOMAIN 152..167 BH2.
FT TRANSMEM 181..198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BFCB65DDA4CA03 CRC64;

Query Match 36.8%; Score 371; DB 1; Length 204;
Best Local Similarity 42.1%; Pred. No. 2.2e-26;
Matches 82; Conservative 25; Mismatches 62; Indels 26; Gaps 4;

QY 10 TRALVADPVGVYKLRQKGYVC-----GAGPEGPAADPLHQAMR 47
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
S SRDLVEKVFVSKLSQ-NEACRKFSNNENPNPYLMEPSGISRPEGATOGIVEEVQLALL 63
QY 48 AAGDEFTFRRTPTSDLAQLHTVPGSAQORFTQVSDPLFOGGPNWGRILVAFVFGALC 107
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 EATGEFFELRYQRAFSDLTSQLHTQDTAQSFOQVMGELFRDGTNWRIVAFPSFRLALC 123
QY 108 AESVKNKEMEPVLVQOVQEMVAYVLETRLADWIISSGGVAEFTALYGDGALEARRLRE--G 165
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 VESANKEMTDLLPRIVQMVNYLEHTLQPMQENGWEAVGLYGXAAAGSRSGERFG 183
QY 166 NMAASVRTVLTGAVAL 180
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:
184 RLITI-VMLTGVFAL 197
```

Search completed: March 25, 2004, 15:43:01
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 15:36:20 ; Search time 14 Seconds
(without alignments)
1326.069 Million cell updates/sec

Title: US-09-155-327g-7

Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADPVG.....LGAVALGALVTGAFPSK 193

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	428.5	42.6	233	2	bcl-x long - mouse
2	428.5	42.6	233	2	apoptosis regulato
3	424.5	42.2	233	2	BCL-X protein - ra
4	423.5	42.1	233	2	transforming prote
5	414	41.1	232	2	S24390
6	412.5	41.0	239	1	TVHJAI
7	412	40.9	236	2	transforming prote
8	407	40.4	236	2	BCL-2 - rat (fragm
9	406	40.3	236	1	gene bcl-2 protein
10	404.5	40.2	233	2	transforming prote
11	403	40.0	236	2	BCL-X-long - rat
12	378	37.5	190	2	apoptosis regulato
13	377.5	37.5	214	2	BCL-X transmembran
14	375.5	37.3	227	2	apoptosis regulato
15	356	35.4	216	2	transforming prote
16	349.5	34.7	199	1	TVMSBI
17	346	34.4	205	1	transforming prote
18	277.5	27.6	154	2	gene bcl-2 protein
19	182	18.1	170	2	BCL-X short - mous
20	176	17.5	211	2	gene bcl-xshort pr
21	174	17.3	176	2	apoptosis regulato
22	173	17.2	211	2	apoptosis regulato
23	157.5	15.6	192	2	BCL-2-associated p
24	153	15.2	192	2	BCL-2-associated p
25	150	14.9	261	2	apoptosis regulato
26	149.5	14.8	133	2	BCL-2-associated p
27	149.5	14.8	133	2	BCL-2-associated p
28	146.5	14.5	179	2	BCL-2-associated p
29	146.5	14.5	218	2	BCL-2-associated p

30	143	14.2	177	2	SS4778	NR-13 protein - qu
31	141	14.0	255	2	UC7567	Mcl-1a protein - z
32	137.5	13.7	143	2	T18921	bcl-2-associated p
33	118	11.7	175	2	T19055	BCL-2 related - hu
34	112	11.1	350	2	A47476	BCL2 homolog MCL1
35	105	10.4	172	2	I49449	hemopoietic-specif
36	91.5	9.1	301	2	T36534	proliferative lipase
37	89	8.8	185	2	B83217	hypothetical prote
38	87	8.6	3433	1	GNWVXV	genome polypeptide
39	85	8.4	270	2	A12598	dihydroadipic acid
40	85	8.4	279	2	B97381	glutamate-ammoma
41	84.5	8.4	358	1	ATLCQB	DNA binding protei
42	83	8.2	417	2	T39939	genome polypeptide
43	82.5	8.2	1440	1	GNWVJF	genome polypeptide
44	82.5	8.2	3432	1	GNWVJF	genome polypeptide
45	81.5	8.1	354	2	SS2040	Gln 1.1 protein -

ALIGNMENTS

```
RESULT 1
149056
bcl-x long - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C:Accession: I49056; S52866
R: Pang, W.; Rivard, J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49055; MUID:95052604; PMID:7963517
A:Accession: I49056
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
A:Cross-references: EMBL:U0101; NID:9506647; PIDN:AAA82173.1; PID:9506648
R: Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu
A:Reference number: S52866
A:Accession: S52866
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-233 <KAM>
A:Cross-references: EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match          42.6%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.9e-32;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 PALVADPVGKLRKQY-----V 28
DB 6 RELVDFSLSYLXSKQGSWSQSPDENRTEAPETAEERETPSAINGNSWMLADSPAV 65
QY 29 CGAGRGESPAD-----PIHQMAAGDEFTRRRPSDAAOLHTWPSAQRFT 80
DB 66 NGA-TGHSLSADAEVTPMAAVKQALREAGDEFLRRRAASDLSQHLTPGAYVSGFE 124
QY 81 QVSDLEFGCGPNMGRALVAFVFGAALCAESVNMKEVLVGVGVNVAAYLETRLADVIHS 140
DB 125 QVAVNELPFDGVNWRIVAFVFGAALCVESVDKMOVLSRIASWMAATYLNDDHEPIQGE 184
QY 141 SGGAAEFTALVGDALREARLRE--GNWASVRLTGAVALGAL 183
DB 185 NGMDTFVDLVGNNAALAESRKQGERFNRWFLTGTVAGVLLGSL 229

RESULT 2
B47537
apoptosis regulator bcl-xL - human
N:Alternate names: bcl-2-related protein
N:Contains: apoptosis regulator bcl-xS
```

C/Species: Homo sapiens (man)
 C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2003
 C/Accession: B47537, C47537
 R/Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
 Cell 74, 597-608, 1993
 A/Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
 A/Reference number: A47537; MUID:93364977; PMID:8358789
 A/Accession: B47537
 A/Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-233 <B01>
 A/Cross-references: GB:L20121; NID:9510900; PIDN:CAA80661.1; PID:9510901
 A/Accession: C47537
 A/Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-69; G, 71-125, 189-233 <B02>
 A/Cross-references: GB:L20122; NID:9623236; PIDN:CAA80662.1; PID:9623237
 C/Genetics:
 A/Gene: GDB:BCL2L
 A/Cross-references: GDB:228079
 A/Superfamily: bcl apoptosis regulator, inhibitory type
 C/Keywords: alternative splicing; apoptosis
 F:1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
 F:1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>

Query Match 42.6%; Score 428.5; DB 2; Length 233;
 Best Local Similarity 40.6%; Pred. No. 2.9e-32;
 Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

11 RLVDVFGYKLRQKGY-----YCGAGP-----GEGPAA 39
 6 RLVDVFLSYKLSQKGSWSQPSDVEENRTAPBGTSEBMTSPAINGNPSMHLADSPAV 65
 40 D-----PLHQAMRAAGDEFEFRFRFTSDLAQLHVTGPSAQGRFTQ 81
 66 NGATAHSSLDAREVTPMAAVKQALREAGDEFEFLRYRAFSLTLSQHLITGTAYQSFQ 125
 82 VSDLEFQGGPMGRVAFVFGALCAESVKNKEMEPVGVQVQEMWVAYLETRLADWTHSS 141
 126 VVNELEFRDGVNMGRIYAFVFGALCVESVDKEMQVLSRIAMWATYLNHLEPWIGEN 165

QY 142 GGMAEFTALYDGALEBARLRRE--GNWASVRYTLTGAVALGAL 183
 DB 186 GGMDFVDELVGNMAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 3
 BCL-X protein - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 28-Jul-2003
 C/Accession: S51761, S51762
 R/Michaelidis, T.M.
 Submitted to the EMBL Data Library, November 1994
 A/Reference number: S51761
 A/Accession: S51761
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-223 <MIC>
 A/Cross-references: EMBL:X82337; NID:9607176; PIDN:CAA57886.1; PID:9607177
 A/Experimental source: embryonic; brain
 A/Accession: S51762
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-125,189-233 <MT2>
 A/Cross-references: EMBL:X82337; NID:9607176; PIDN:CAA57887.1; PID:9607178
 A/Experimental source: embryonic; brain
 A/Note: smaller form due to splicing
 C/Genetics:
 A/Introns: 125/3
 C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.2%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 6.7e-32;
 Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 13 LVNDFYGYKLRQKGY-----YCG 30
 DB 8 LVNDFLSYKLSQKGSWSQPSDVEENRTAPBGTSEBMTSPAINGNPSMHLADSPAVNG 67
 QY 31 AGPEGPAAAD-----PLHQAMRAAGDEFEFRFRFTSDLAQLHVTGPSAQGRFTQV 82
 DB 68 A-TGSHSSLDAREVTPMAAVKQALREAGDEFEFLRYRAFSLTLSQHLITGTAYQSFQV 126
 QY 83 SDELFGGPMGRVAFVFGALCAESVKNKEMEPVGVQVQEMWVAYLETRLADWTHSSG 142
 DB 127 VVNELEFRDGVNMGRIYAFVFGALCVESVDKEMQVLSRIAMWATYLNHLEPWIGEN 186

QY 143 GGMAEFTALYDGALEBARLRRE--GNWASVRYTLTGAVALGAL 183
 DB 187 GGMDFVDELVGNMAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 4
 A37332
 transforming protein (bcl-2-alpha) - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
 C/Accession: A37332; S35453
 R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari-
 A/Reference number: A37332; MUID:9235724; PMID:1508712
 A/Accession: A37332
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-233 <EGU>
 A/Cross-references: EMBL:D11381
 C/Genetics:
 A/Introns: 189/3
 A/Superfamily: bcl apoptosis regulator, inhibitory type
 C/Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.1%; Score 423.5; DB 2; Length 233;
 Best Local Similarity 38.0%; Pred. No. 8.3e-32;
 Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;

QY 9 DTRLVADVFGYKLRQKGYVCGAG-----PGECPAADP----- 41
 DB 10 DNRSEIVLKYTHYKLSQKGSQGYDMAAGEDRPVPAPAPAAVAAGAASHRPEPPGSA 69
 QY 42 -----LHQAMRAAGDEFEFRFRFTSDLAQLHVTGPSAQGRFTQVSD 84
 DB 70 AASEVFPAGELRAPPGVHIALROAGDEFRRYORDFAQMSQHLTPTAGRFVAVVE 129

QY 85 ELFGGPMGRVAFVFGALCAESVKNKEMEPVGVQVQEMWVAYLETRLADWTHSSG 144
 DB 130 ELFRDGVNMGRIYAFVFGALCVESVKNKEMEPVGNINATWTEYLNRLHMIQDNGW 189

QY 145 AEFTALYDGALEBARLRREGNWASVRYTLTGAVALGAVTGAFPAASK 193
 DB 190 DAFVELYGN---SNRPFLDFPSWISLKLTL--LVVGACITTGAYIGHK 233

RESULT 5
 S24390
 transforming protein (bcl-2) homolog - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 28-Jul-2003
 C/Accession: S24390
 R/Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
 Biochim. Biophys. Acta 1137, 109-113, 1992
 A/Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
 A/Reference number: S24390; MUID:92379084; PMID:1511008
 A/Accession: S24390
 A/Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-232 <CAZ>
 A:Cross-references: EMBL:Z11961; NID:g62969; PIRN:CAA78018.1; PID:g62970
 C:Superfamily: bcl apoptosis regulator, inhibitory type
 C:Keywords: mitochondrion; transmembrane protein

Query Match 41.1%; Score 414; DB 2; Length 232;
 Best Local Similarity 37.7%; Pred. No. 6.3e-31;
 Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

QY 9 DTRALVADVFVGYLRLKRGVCCAG-----PGEGRADP----- 41
 Db 10 DNRREIVKXIHXYLSORGYEMDAGEDRPVPAPAPAAVAAAGASSHHRPSAPRL 69
 QY 42 -----LHQAMRAAGDEFEFRPRRTSDLAALHTTPGSAOQRFQVDE 85
 Db 70 LTVRCRLRGCAAPGVGHALRQAGDFSRRYQDFPAQMSQGLHLPFATGRFVAAYVE 129
 QY 86 LFGGPNMGRILVAFVFGAALCAESVNMKEPPLVGQVQEMVAVYLETRLADWISSGGMA 145
 Db 130 LTRDGNVWRIVAFPEFGVCMCVESVNRMSPLVDNIAATMTREYLNRLHNMWIDNGMD 189
 QY 146 EFTALYGDGALAEARLRGNMNASVTVLTGAVALGALVTGAFPAASK 193
 Db 190 AFEVLEYGN-----SMRPLDFFSWISLKTILSL-LVVGACITLGAYLGHK 232

RESULT 6

Transferring protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1986 #sequence revision 07-Jun-1996 #text change 28-Jul-2003
 C:Accession: C37332; A29409; S02452; A24428; A27622; B27622
 R:Gnughl, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
 A:Reference number: A37332; MUID:92257524; PMID:1508712

A:Accession: C37332
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA

A:Residues: 1-239 <EGU>
 A>Note: this report is a correction
 R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
 A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene for the B-cell lymphoma cell growth factor
 A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: A29409
 A:Molecule type: mRNA

A:Residues: 1-95, 'A', 'G', '111-236', 'S', '238-239' <TSU>
 A:Cross-references: GB:M13994; NID:g179366; PIRN:AAA5183.1; PID:g179367
 A>Note: this sequence has been corrected in reference A37332
 R:Sefto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
 EMBO J. 7, 123-131, 1988

A:Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2 gene
 A:Reference number: S02452; MUID:88196071; PMID:2834197

A:Accession: S02452
 A:Molecule type: mRNA

A:Residues: 1-239 <SET>
 R:Clay, M.L.; Smith, S.D.; Sklar, J.

Cell 47, 19-28, 1986
 A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain enhancer
 A:Reference number: A24428; MUID:87002488; PMID:2875799

A:Accession: A24428
 A:Molecule type: mRNA

A:Residues: 1-58, 'T', '60-116', 'R', '118-239' <CLB>
 A:Cross-references: GB:M14745; NID:g179370; PIRN:AAA35591.1; PID:g179371
 R:Hu, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakkeni, A.
 Oncogene Res. 2, 263-275, 1988

A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: a study of 100 cases
 A:Reference number: A27622; MUID:88217344; PMID:3285301

A:Accession: A27622
 A:Molecule type: mRNA

A:Residues: 1-58, 'T', '60-239' <HUA>

A:Accession: B27622
 A:Molecule type: DNA
 A:Residues: 1-6, 'S', '8-58', 'T', '60-128', 'C', '130-239' <HUA>
 A>Note: the sequence was determined from the germ-line gene
 C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
 C:Genetics:
 A:Gene: GDB:BCL2
 A:Cross-references: GDB:119031; OMIM:151430
 A:Map position: 18q21.3-18q21.3

C:Function:
 A:Description: blocks apoptosis in hematopoietic cells
 C:Superfamily: bcl apoptosis regulator, inhibitory type
 C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 41.0%; Score 412.5; DB 1; Length 239;
 Best Local Similarity 37.0%; Pred. No. 9e-31;
 Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

QY 9 DTRALVADVFVGYLRLKRGVCCAG-----PGE----- 35
 Db 10 DNRREIVKXIHXYLSORGYEMDAGDVGAPGAPGIFSSQPGHTPAPASRDPAVART 69
 QY 36 -----GPAADP-----LHQAMRAAGDEFEFRPRRTSDLAALHTTPGSAOQRF 78
 Db 70 SPLTPAPAPGAAAPLSPVPVHLTLRQAGDFSRRYQDFPAQMSQGLHLPFATGRFVAAYVE 129
 QY 79 FTVSDELFGGPNMGRILVAFVFGAALCAESVNMKEPPLVGQVQEMVAVYLETRLADWISSGGMA 138
 Db 130 FATVEELFRDGNVWRIVAFPEFGVCMCVESVNRMSPLVDNIAATMTREYLNRLHNMWIDNGMD 189
 QY 139 HSSGGNAEFTALYGDGALAEARLRGNMNASVTVLTGAVALGALVTGAFPAASK 193
 Db 190 QDNGMDAFVLEYG-----PSMRPLDFFSWISLKTILSL-LVVGACITLGAYLGHK 239

RESULT 7

BCL-2 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text change 28-Jul-2003
 C:Accession: I67432
 R:Tilly, U.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995

A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin
 constitutive bcl-2 and bcl-2-like messenger ribonucleic acid levels.

A:Reference number: I53295; MUID:95129487; PMID:7828536

A:Accession: I67432

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-236 <RES>

A:Cross-references: EMBL:U34964; NID:g1004378; PIRN:AAA77687.1; PID:g1004379
 C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.9%; Score 412; DB 2; Length 236;
 Best Local Similarity 36.2%; Pred. No. 9.8e-31;
 Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADVFVGYLRLKRGV-----PGE----- 27
 Db 10 DNRREIVKXIHXYLSORGYEMDAGEDSDAPLRAPPGIFSQPESNRPVAVRDTAART 69
 QY 28 -----VCGAGPEGEPAADPLHQAMRAAGDEFEFRPRRTSDLAALHTTPGSAOQRF 81
 Db 70 SPLRPLVANAAGPLSPVPVHLTLRQAGDFSRRYQDFPAQMSQGLHLPFATGRFAT 129
 QY 82 VSDLELFGGPNMGRILVAFVFGAALCAESVNMKEPPLVGQVQEMVAVYLETRLADWISSGGMA 141
 Db 130 VYBELFRDGNVWRIVAFPEFGVCMCVESVNRMSPLVDNIAATMTREYLNRLHNMWIDNGMD 189
 QY 142 GGAETALYGDGALAEARLRGNMNASVTVLTGAVALGALVTGAFPAASK 193
 Db 190 GGMDAFVLEYG-----PSMRPLDFFSWISLKTILSL-LVVGACITLGAYLGHK 236

A/Gene: bcl-2
C/Superfamily: bcl apoptosis regulator, inhibitory type
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-214 <RES>
A/Cross-references: EMBL:U01012; NID:g506649; PIDN:AAA2174.1; PID:g506650
C/Genetics:
A/Gene: bcl-x-long
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.8%; Score 403; DB 2; Length 236;
Best Local Similarity 35.3%; Pred. No. 6,7e-30;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;

QY 9 DTRALVADFGYKLRQKGY-----VCGAGPREGP----- 27
DB 10 DNRIRVWKYTHYKLSQRYGWDVDVDAAPLGAAPTPGIFSFPESNPTPAVRDMAART 69
QY 28 -----VCGAGPREGPADPLHQAMRAAGDEFETFRPTSDLAOLHTVPGSAQORFTQ 81
DB 70 SLPRLVATTGPTLSPVPVVALTLRRAGDPSRRIRRDPAEMSSQLHTPTGARGHAT 129
QY 82 VSDELFOGQPNWGRIVAFVFGAALCAESYVKEMEPVGVQOEMWVAYLETRLADWIHS 141
DB 130 VVELLFRDGVNWGRIVAFERGVVVCESVNRKMSPLVDNIALMTEYLNRHLHTWIGDN 189
QY 142 GGALEFTALYGDGALAEARLRREGNMAVTRVLTGAVALALVTVGAFFASK 193
DB 190 GGMDAFELYG-----PSVRPLDFPSWLSLTKTLIAL-VGACITLGYLGHK 236

RESULT 12

A47537
apoptosis regulator bcl-x - chicken
C/Species: Gallus gallus (chicken)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 28-Jul-2003
C/Accession: A47537
R/Bolise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A/Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A/Reference number: A47537; MUID:93364977; PMID:8358789
A/Accession: A47537
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-190 <BS1>
A/Cross-references: GB:223110; GB:L20120; NID:g510898; PIDN:CAA0657.1; PID:g510899
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.5%; Score 378; DB 2; Length 190;
Best Local Similarity 43.8%; Pred. No. 1.1e-27;
Matches 81; Conservative 14; Mismatches 44; Indels 46; Gaps 3;

QY 11 RALVADFGYKLRQKGY-----VCGAGPREGP----- 37
DB 6 RELVIDFVSYKLSQRGHWELEEDENRTDTAAEAMDSVLNGSPWHPAGVNVGAT 65
QY 38 -----AADPLHQAMRAAGDEFETFRPTSDLAOLHTVPGSAQORFTQVSD 85
DB 66 VHRSSLEVHEIVRASDVQALRDAGDEFELRYRASFDTLSQLHTPTGIVQSFEOVNE 125
QY 86 LFOGQPNWGRIVAFVFGAALCAESYVKEMEPVGVQOEMWVAYLETRLADWIHS 145
DB 126 LPHGVNWGRIVAFVFGAALCAESYVKEMEPVGVQOEMWVAYLETRLADWIHS 185
QY 146 EFTAL 150
DB 186 R-TAL 189

RESULT 13

bcl-x transmembrane deleted - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C/Accession: I49057
R/Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A/Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A/Reference number: I49055; MUID:95052604; PMID:7963517

A/Accession: I49057
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-214 <RES>
A/Cross-references: EMBL:U01012; NID:g506649; PIDN:AAA2174.1; PID:g506650
C/Genetics:
A/Gene: bcl-x-long
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.5%; Score 377.5; DB 2; Length 214;
Best Local Similarity 42.8%; Pred. No. 1.4e-27;
Matches 80; Conservative 16; Mismatches 40; Indels 51; Gaps 3;

QY 11 RALVADFGYKLRQKGY-----VCGAGPREGP----- 28
DB 6 RELVIDFVSYKLSQRYGWSQFSDVEENRTAEPETEARETTPSAINGNPSMHLADSPAV 65
QY 29 CGAGPREGPAD-----PLHQAMRAAGDEFETFRPTSDLAOLHTVPGSAQORFT 80
DB 66 NGA-TGHSSLDAREVITMAAVKQALREAGDEFELRYRASFDTLSQLHTPTGIVQSF 124
QY 81 QVSDELFOGQPNWGRIVAFVFGAALCAESYVKEMEPVGVQOEMWVAYLETRLADWIHS 140
DB 125 QVNNELFRDGVNWGRIVAFERGVVVCESVNRKMSPLVDNIALMTEYLNRHLHTWIGDN 184
QY 141 SGGMAEF 147
DB 185 NGGMDTF 191

RESULT 14

JEB0203
apoptosis regulator bcl-x isoform - human
N/Alternate names: h-bcl-xbeta
C/Species: Homo sapiens (man)
C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 28-Jul-2003
C/Accession: JEB0203
R/Ban, U.; Bocharov, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A/Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A/Reference number: JEB0203; MUID:98340865; PMID:9675101
A/Accession: JEB0203
A/Molecule type: mRNA
A/Residues: 1-227 <BAN>
A/Cross-references: GB:U72398; NID:g1622940; PIDN:AAH17354.1; PID:g1622941
C/Genetics:
A/Gene: bcl-x
A/Map position: 20
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.3%; Score 375.5; DB 2; Length 227;
Best Local Similarity 40.8%; Pred. No. 2.3e-27;
Matches 82; Conservative 18; Mismatches 50; Indels 51; Gaps 3;

QY 11 RALVADFGYKLRQKGY-----VCGAGPREGP----- 28
DB 6 RELVIDFVSYKLSQRYGWSQFSDVEENRTAEPETEARETTPSAINGNPSMHLADSPAV 65
QY 29 CGAGPREGPAD-----PLHQAMRAAGDEFETFRPTSDLAOLHTVPGSAQORFT 80
DB 66 NGA-TGHSSLDAREVITMAAVKQALREAGDEFELRYRASFDTLSQLHTPTGIVQSF 124
QY 81 QVSDELFOGQPNWGRIVAFVFGAALCAESYVKEMEPVGVQOEMWVAYLETRLADWIHS 140
DB 125 QVNNELFRDGVNWGRIVAFERGVVVCESVNRKMSPLVDNIALMTEYLNRHLHTWIGDN 184
QY 141 SGGMAEF 147
DB 185 NGGMDTF 191

RESULT 15

B37332

transforming protein (bcl-2-beta) - chicken

C/Species: Gallus gallus (chicken)

C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003

C/Accession: B37332; S35452

R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A/Reference number: A37332; MUID:92375724; PMID:1508712

A/Accession: B37332

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-216 <ESU>

A/Cross-references: EMBL:D11381; EMBL:D11382

C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 35.4%; Score 356; DB 2; Length 216;

Best Local Similarity 38.4%; Pred. No. 1,4e-25;

Matches 71; Conservative 21; Mismatches 49; Indels 44; Gaps 2;

QY 9 DTRALVADPVGKLRQKGYVCGAG-----PGECPADP----- 41

Db 10 DNRKIVLKTIHYKLSQKGYDMAAGBDRPPVPAPAPAPAAVAAAGASSHRRPPGSA 69

QY 42 -----LHQMRAGDEFEFRFRFTSDLAQLHTPGSAOQRFTOVSD 84

Db 70 AASEVPPEAGLRAPRPPGVHLLRQAGDEFRRYQRDPQMSQGLHTPTAHGRFVAAYE 129

QY 85 ELFGGPNMGRLLVAFVFGAALCAESYNKEMEPVGVQVQEMWVAYLETRLADMIHSSGM 144

Db 130 ELFRDGVNMGRIYVAFEFEGVMCVESYNREMSPLVDNIATWTEYLNRLHNWIQDNGM 189

QY 145 AEFTA 149

Db 190 VRACA 194

Search completed: March 25, 2004, 15:45:06
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 15:19:05 ; Search time 51 Seconds
(without alignments)
1069.248 Million cell updates/sec

Title: US-09-155-327G-7
Perfect score: 1007
Sequence: 1 MATPAPASPDTRALVADPEVY.....LTGAVALGALVTYGAFFAPK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_290Jan04:*
1: geneseqp1360s:*
2: geneseqp1390s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	100.0	193	2	AAV05530
2	1007	100.0	193	7	ADDA6742
3	1002	99.5	193	2	AAW61392
4	1002	99.5	193	2	AAW61392
5	1000	99.3	193	2	AAW61392
6	1000	99.3	193	2	AAW61392
7	1000	99.3	193	2	AAW61392
8	997	98.9	193	2	AAW61392
9	996	98.9	193	2	AAW61392
10	996	98.9	193	2	AAW61392
11	991	98.4	192	2	AAW61392
12	958.5	95.2	192	2	AAW61392
13	867	86.1	166	5	AAW61392
14	821.5	81.6	166	5	AAW61392
15	766	76.1	166	5	AAW61392
16	766	76.1	166	5	AAW61392
17	766	76.1	166	5	AAW61392
18	433.5	43.0	411	4	AAU00219
19	433.5	42.9	411	4	AAU00219
20	428.5	42.6	233	2	AAW61392
21	428.5	42.6	233	2	AAW61392
22	428.5	42.6	233	2	AAW61392
23	428.5	42.6	233	2	AAW61392
24	428.5	42.6	233	2	AAW61392
25	428.5	42.6	233	2	AAW61392

25	428.5	42.6	233	4	AAW61392	AAW61392
27	428.5	42.6	233	4	AAW61392	AAW61392
28	428.5	42.6	233	4	AAW61392	AAW61392
29	428.5	42.6	233	4	AAW61392	AAW61392
30	428.5	42.6	233	4	AAW61392	AAW61392
31	428.5	42.6	233	4	AAW61392	AAW61392
32	428.5	42.6	233	4	AAW61392	AAW61392
33	428.5	42.6	233	4	AAW61392	AAW61392
34	428.5	42.6	233	4	AAW61392	AAW61392
35	424.5	42.2	233	4	AAW61392	AAW61392
36	416.5	41.4	239	4	AAW61392	AAW61392
37	415.5	41.3	152	6	AAW61392	AAW61392
38	413	41.0	236	4	AAW61392	AAW61392
39	413	41.0	236	4	AAW61392	AAW61392
40	412.5	41.0	239	4	AAW61392	AAW61392
41	412.5	41.0	239	4	AAW61392	AAW61392
42	412.5	41.0	239	4	AAW61392	AAW61392
43	412.5	41.0	239	4	AAW61392	AAW61392
44	412.5	41.0	239	4	AAW61392	AAW61392
45	412.5	41.0	239	4	AAW61392	AAW61392

ALIGNMENTS

RESULT 1
ID AAV05530
AAV05530 standard; protein; 193 AA.

AC AAV05530;
DT 05-JUL-1999 (first entry)
XX Human Bcl-w protein essential for spermatogenesis.
XX Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
XX animal model.
XX Homo sapiens.
OS Homo sapiens.
PN WO9913710-A1.
XX 25-MAR-1999.
PD 16-SEP-1998; 98MO-AU000764.
XX 16-SEP-1997; 97AU-00009228.
XX 16-SEP-1997; 97AU-00009228.
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX Cory S, Adams J, Print C, Gibson L, Koentgen F,
XX WPI; 1999-243890/20.
XX N-PSDB; AAX25132.
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w.
XX Claim 2; Page 33; 52pp; English.
XX The present sequence is human Bcl-w, a pro-survival member of the Bcl-2
XX family which is widely expressed and which is essential for
XX spermatogenesis. The invention relates generally to a method of treatment
XX and to an animal model for the identification of molecules and genetic
XX sequences useful for inducing or reducing fertility of male animals.
XX Methods are provided for the treatment of infertility, or for reducing
XX fertility, by modulating spermatogenesis. An animal model carries a
XX mutation in at least one allele of the human or murine bcl-w gene (see
XX AAX25132-35) or in a gene associated with bcl-w. Such animals have
XX disorganized seminiferous tubules and are substantially infertile, but
XX possess no other major abnormalities as determined by histological
XX examination. They can be used to screen for therapeutic molecules
XX including genetic sequences capable of inducing, enhancing or otherwise

CC facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ Sequence 193 AA;

Query Match 100.0%; Score 1007; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1,4e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPEGPAADPLHQAARAAGDEFEFRFRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPEGPAADPLHQAARAAGDEFEFRFRRT 60
QY 61 FSDLAAGLHVTGSAQGRFTQVSDLEFGGPNMGRILVAFVFGALCAESVNMKEPVLVG 120
DB 61 FSDLAAGLHVTGSAQGRFTQVSDLEFGGPNMGRILVAFVFGALCAESVNMKEPVLVG 120
QY 121 QVQEMWVAYLETRLADWTHSSGWAFFETALYGDALBEARLRREGWNASVRYTLTGAVALL 180
DB 121 QVQEMWVAYLETRLADWTHSSGWAFFETALYGDALBEARLRREGWNASVRYTLTGAVALL 180
QY 181 GALVTGAFPFASK 193
DB 181 GALVTGAFPFASK 193

RESULT 2
ADD6742
ID ADD6742 standard; protein; 193 AA.

XX ADD6742;
AC
XX 29-JAN-2004 (first entry)
DE Human Protein Q92843, SEQ ID NO 12427.
XX
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
OS Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI, 2003-268312/26.
DR GENBANK; Q92843.

XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

Query Match 100.0%; Score 1007; DB 7; Length 193;
Best Local Similarity 100.0%; Pred. No. 1,4e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPEGPAADPLHQAARAAGDEFEFRFRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGPEGPAADPLHQAARAAGDEFEFRFRRT 60
QY 61 FSDLAAGLHVTGSAQGRFTQVSDLEFGGPNMGRILVAFVFGALCAESVNMKEPVLVG 120
DB 61 FSDLAAGLHVTGSAQGRFTQVSDLEFGGPNMGRILVAFVFGALCAESVNMKEPVLVG 120
QY 121 QVQEMWVAYLETRLADWTHSSGWAFFETALYGDALBEARLRREGWNASVRYTLTGAVALL 180
DB 121 QVQEMWVAYLETRLADWTHSSGWAFFETALYGDALBEARLRREGWNASVRYTLTGAVALL 180
QY 181 GALVTGAFPFASK 193
DB 181 GALVTGAFPFASK 193

RESULT 3

AAW61392
ID AAW61392 standard; protein; 193 AA.

XX AAW61392;

XX 02-OCT-1998 (first entry)

XX Human bcl-y protein.

XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

XX Homo sapiens.

XX US5789201-A.

XX 04-AUG-1998.

XX 11-FEB-1997; 97US-00798897.

XX 23-FEB-1996; 96US-0012201P.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI, 1998-446079/38.
DR N-PSDB; AAV28334.

XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.

PT cancers.
 XX
 PS Example; Column 17/18; 27pp; English.
 XX
 CC The mammalian bcl-2 protein is a member of the bcl-2 family, components
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity
 CC and the apoptosis blocking activity. bcl-2 falls in the apoptosis
 CC actively category. The recombinant protein may be used to prevent
 CC uncontrolled cell growth, either by its direct administration to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired
 CC
 XX Sequence 193 AA;
 SQ
 Query Match 99.5%; Score 1002; DB 2; Length 193;
 Best Local Similarity 99.5%; Pred. No. 5e-102;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MATPASADPTALVADPFGYKLRQKGYVCGAGPBGSPADPLHOMARAAGDEFFTRFRRT 60
 DB 1 MATPASADPTALVADPFGYKLRQKGYVCGAGPBGSPADPLHOMARAAGDEFFTRFRRT 60
 QY 61 FSDLAQLHTVTPGSAQCRFTQVSDLPFGGPNMGRIVAFVFGALCAESVKNKMEPLVG 120
 DB 61 FSDLAQLHTVTPGSAQCRFTQVSDLPFGGPNMGRIVAFVFGALCAESVKNKMEPLVG 120
 QY 121 QVQEMWVAVLETRLADWTHSSGGMAEFTALYDGLAEARLRREGNMAVTRVLTGAVAL 180
 DB 121 QVQEMWVAVLETRLADWTHSSGGMAEFTALYDGLAEARLRREGNMAVTRVLTGAVAL 180
 QY 181 GALVTGAFPAK 193
 DB 181 GALVTGAFPAK 193
 RESULT 4
 AAM97392
 ID AAM97392 standard; protein; 193 AA.
 AC AAM97392;
 XX
 XX 20-MAY-1999 (first entry)
 XX
 DE The human bcl-2 protein.
 XX
 XX Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune disease; parasite.
 XX
 OS Homo sapiens.
 XX
 XX US5883229-A.
 XX
 XX 16-MAR-1999.
 XX
 XX 25-NOV-1997; 97US-00978523.
 XX
 XX 23-FEB-1996; 96US-0012201P.
 XX
 XX 11-FEB-1997; 97US-00798897.
 XX
 XX (COCE-) COCESENS INC.
 XX
 XX Guastella J;
 XX
 XX WPI; 1999-214150/18.
 XX
 XX N-PSDB; AAX15946.
 XX
 PT Novel bcl-2 homologues of the rat and human bcl-2 protein - useful for

PT modulating programmed cell death.
 XX
 PS Claim 1; Col 17-18; 26pp; English.
 XX
 CC The present sequence represents human bcl-2 protein (Hbcl-2). The
 CC specification also describes rat bcl-2 protein (Rbcl-2). Rbcl-2 and Hbcl-
 CC y are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from strokes, head trauma,
 CC Alzheimer's disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
 CC - conditions where cells under go premature cell death as a result of
 CC triggers which may or may not be apparent. They may also be used in this
 CC way to develop cell lines which remain viable in culture for an extended
 CC period. In contrast, if they act as cell death stimulators, Rbcl-2 and
 CC Hbcl-2 may be used to treat conditions associated with prolonged cell
 CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
 CC and auto/hyperimmune diseases. They may also be used to cause cell death
 CC in, and hence control, parasites
 CC
 XX Sequence 193 AA;
 SQ
 Query Match 99.5%; Score 1002; DB 2; Length 193;
 Best Local Similarity 99.5%; Pred. No. 5e-102;
 Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MATPASADPTALVADPFGYKLRQKGYVCGAGPBGSPADPLHOMARAAGDEFFTRFRRT 60
 DB 1 MATPASADPTALVADPFGYKLRQKGYVCGAGPBGSPADPLHOMARAAGDEFFTRFRRT 60
 QY 61 FSDLAQLHTVTPGSAQCRFTQVSDLPFGGPNMGRIVAFVFGALCAESVKNKMEPLVG 120
 DB 61 FSDLAQLHTVTPGSAQCRFTQVSDLPFGGPNMGRIVAFVFGALCAESVKNKMEPLVG 120
 QY 121 QVQEMWVAVLETRLADWTHSSGGMAEFTALYDGLAEARLRREGNMAVTRVLTGAVAL 180
 DB 121 QVQEMWVAVLETRLADWTHSSGGMAEFTALYDGLAEARLRREGNMAVTRVLTGAVAL 180
 QY 181 GALVTGAFPAK 193
 DB 181 GALVTGAFPAK 193
 RESULT 5
 AAM36047
 ID AAM36047 standard; protein; 193 AA.
 AC AAM36047;
 XX
 XX 22-APR-1998 (first entry)
 XX
 DE Human bcl-2 protein.
 XX
 XX Bcl-2; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 KW diagnosis; degenerative disease.
 XX
 XX Homo sapiens.
 XX
 XX WO9735971-A1.
 XX
 XX 02-OCT-1997.
 XX
 XX 27-MAR-1997; 97WO-AU000199.
 XX
 XX 27-MAR-1996; 96AU-00008965.
 XX
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 XX Cory S, Adams JM, Gibson LM, Holmgren SP;
 XX

DR WPI, 1997-489635/45.
 DR N-PSDB; AAY96577.
 XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.
 PS Claim 6; Page 48; 86pp; English.
 XX This sequence represents a novel human protein, bcl-w, encoded by the bcl
 CC -2 gene family and extracted from an adult brain library. This gene
 CC promotes cell survival, so its modulation is useful in treatment of
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
 CC ischaemia, human immunodeficiency virus infection or in cell transplants.
 CC Up-regulation of the gene can also be used to modify cell lines cultured
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators
 CC
 SQ Sequence 193 AA;
 Query Match 99.3%; Score 1000; DB 2; Length 193;
 Best Local Similarity 99.0%; Pred. No. 8.3e-102;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MATPSADPTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFEFRFRRT 60
 Db 1 MATPSADPTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFEFRFRRT 60
 QY 61 FSDLAQLHTVPGSAQQRFTQVSDLPFGGPNWGRVAFVFGAALCAESVKNKEBPLVG 120
 Db 61 FSDLAQLHTVPGSAQQRFTQVSDLPFGGPNWGRVAFVFGAALCAESVKNKEBPLVG 120
 QY 121 QVQEMWVAVLETRLADWTHSSGGMAEFTALYDGDALAEARRLRGNWASVTVLTGAVAL 180
 Db 121 QVQEMWVAVLETRLADWTHSSGGMAEFTALYDGDALAEARRLRGNWASVTVLTGAVAL 180
 QY 181 GALVTVGAFPAK 193
 Db 181 GALVTVGAFPAK 193
 RESULT 6
 AAY05532
 ID AAY05532 standard; protein, 193 AA.
 AC AAY05532;
 DT 05-JUL-1999 (first entry)
 DE Human Bcl-w protein essential for spermatogenesis.
 XX Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
 KW animal model.
 OS Homo sapiens.
 XX MO9913710-A1.
 XX 25-MAR-1999.
 XX 16-SEP-1998; 98WO-AU000764.
 XX 16-SEP-1997; 97AU-00009228.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX Cory S, Adams J, Print C, Gibson L, Koentgen F;
 PI WPI, 1999-243890/20.
 DR N-PSDB; AAX25134.

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 XX Disclosure; Page 37; 52pp; English.
 XX The present sequence is described of a derivative of human Bcl-w (see
 CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation in at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 CC
 SQ Sequence 193 AA;
 Query Match 99.3%; Score 1000; DB 2; Length 193;
 Best Local Similarity 99.0%; Pred. No. 8.3e-102;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MATPSADPTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFEFRFRRT 60
 Db 1 MATPSADPTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFEFRFRRT 60
 QY 61 FSDLAQLHTVPGSAQQRFTQVSDLPFGGPNWGRVAFVFGAALCAESVKNKEBPLVG 120
 Db 61 FSDLAQLHTVPGSAQQRFTQVSDLPFGGPNWGRVAFVFGAALCAESVKNKEBPLVG 120
 QY 121 QVQEMWVAVLETRLADWTHSSGGMAEFTALYDGDALAEARRLRGNWASVTVLTGAVAL 180
 Db 121 QVQEMWVAVLETRLADWTHSSGGMAEFTALYDGDALAEARRLRGNWASVTVLTGAVAL 180
 QY 181 GALVTVGAFPAK 193
 Db 181 GALVTVGAFPAK 193
 RESULT 7
 AAY05531
 ID AAY05531 standard; protein, 193 AA.
 AC AAY05531;
 DT 05-JUL-1999 (first entry)
 DE Mouse Bcl-w protein essential for spermatogenesis.
 XX Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 KW animal model.
 OS Mus sp.
 XX MO9913710-A1.
 XX 25-MAR-1999.
 XX 16-SEP-1998; 98WO-AU000764.
 XX 16-SEP-1997; 97AU-00009228.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX Cory S, Adams J, Print C, Gibson L, Koentgen F;
 PI WPI, 1999-243890/20.

DR N-PSDB; AAX25133.
 XX An animal model exhibiting reduced levels of a bcl-w protein and/or
 PT protein associated with bcl-w.
 XX
 XX Claim 2; Page 35; 52pp; English.
 XX
 CC The present sequence is mouse bcl-w, a pro-survival member of the bcl-2
 CC family which is widely expressed and which is essential for
 CC spermatogenesis. The invention relates generally to a method of treatment
 CC and to an animal model for the identification of molecules and genetic
 CC sequences useful for inducing or reducing fertility of male animals.
 CC Methods are provided for the treatment of infertility, or for reducing
 CC fertility, by modulating spermatogenesis. An animal model carries a
 CC mutation in at least one allele of the human or mouse bcl-w gene (see
 CC AAX25133-35) or in a gene associated with bcl-w. Such animals have
 CC disorganized seminiferous tubules and are substantially infertile, but
 CC possess no other major abnormalities as determined by histological
 CC examination. They can be used to screen for therapeutic molecules
 CC including genetic sequences capable of inducing, enhancing or otherwise
 CC facilitating spermatogenesis in animals, or which can induce infertility
 CC
 XX Sequence 193 AA;
 SQ
 Query Match 99.3%; Score 1000; DB 2; Length 193;
 Best Local Similarity 99.0%; Pred. No. 8.3e-102;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTPASAPDTALVADPFGYGLRQKGYVCGAGPESGPAADPLHQAAMRAGDEFETRRRT 60
 DB 61 FSDLAQLHTVTPGSAOQRFVSDVDELFOGSPNMGRLVAFVFGALCAESVNKMEPLVQ 120
 QY 121 QVQEMWVAYLETRLDWVHSSGMAEFTLYGDGALBEARLRREGNMAVRYTLTGAVALG 180
 DB 121 QVQDMWVAYLETRLDWVHSSGMAEFTLYGDGALBEARLRREGNMAVRYTLTGAVALG 180
 QY 181 GALVTGAFPAASK 193
 DB 181 GALVTGAFPAASK 193
 DB
 RESULT 8
 AAM97394
 ID AAM97394 standard; protein; 192 AA.
 XX
 AC AAM97394;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE Mammalian bcl-y protein.
 XX
 KW Rat bcl-y protein; Bcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 XX
 OS Mammalia.
 XX
 PN US5883229-A.
 XX
 PD 16-MAR-1999.
 XX
 PF 25-NOV-1997; 97US-00978523.
 XX
 PR 23-FEB-1996; 96US-0012201P.
 PR 11-FEB-1997; 97US-00798897.

XX
 PA (COCE-) COCENSYS INC.
 XX
 PI Guastella J;
 XX
 DR WPI, 1999-214150/18.
 XX
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
 PT modulating programmed cell death.
 XX
 PS Claim 2; Col 19-22; 26pp; English.
 XX
 CC The present sequence represents a mammalian bcl-y protein. The
 CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis- conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent. They
 CC may also be used in this way to develop cell lines which remain viable in
 CC culture for an extended period. In contrast, if they act as cell death
 CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites
 CC
 XX Sequence 192 AA;
 SQ
 Query Match 99.0%; Score 997; DB 2; Length 192;
 Best Local Similarity 99.5%; Pred. No. 1.8e-101;
 Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ATPASAPDTALVADPFGYGLRQKGYVCGAGPESGPAADPLHQAAMRAGDEFETRRRT 61
 DB 1 ATPASAPDTALVADPFGYGLRQKGYVCGAGPESGPAADPLHQAAMRAGDEFETRRRT 60
 QY 62 SDLAQLHTVTPGSAOQRFVSDVDELFOGSPNMGRLVAFVFGALCAESVNKMEPLVQ 121
 DB 61 SDLAQLHTVTPGSAOQRFVSDVDELFOGSPNMGRLVAFVFGALCAESVNKMEPLVQ 120
 QY 122 QVQEMWVAYLETRLDWVHSSGMAEFTLYGDGALBEARLRREGNMAVRYTLTGAVALG 181
 DB 121 QVQDMWVAYLETRLDWVHSSGMAEFTLYGDGALBEARLRREGNMAVRYTLTGAVALG 180
 QY 182 ALVTGAFPAASK 193
 DB 181 ALVTGAFPAASK 192
 DB
 RESULT 9
 AAM61391
 ID AAM61391 standard; protein; 193 AA.
 XX
 AC AAM61391;
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Rat bcl-y protein.
 XX
 KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
 XX
 OS Rattus sp.
 XX
 PN US5789201-A.
 XX
 PD 04-AUG-1998.
 XX
 PR 11-FEB-1997; 97US-00798897.

XX 23-FEB-1996; 96US-0012201P.
PR (COCE-) COCENSYS INC.
XX Guastella J;
XX MPI; 1998-446079/38.
XX N-PSDB; AAV28333.
DR
XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.
PT cancers.
XX
XX Example; Fig 3A; 27pp; English.
XX
XX The mammalian bcl-2 protein is a member of the bcl-2 family, components
CC in the cell death pathway. The bcl-2 family have both apoptotic activity
CC and the apoptosis blocking activity. bcl-2 falls in the apoptosis
CC activity category. The recombinant protein may be used to prevent
CC uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired
XX
SQ Sequence 193 AA;
Query Match 98.9%; Score 996; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.3e-101;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASAPTRALVADPFGVYKLRQKGYVCGAGPESGPAADPHQAMRAAGDEFETFRRT 60
1 MATPASPTDTRALVADPFGVYKLRQKGYVCGAGPESGPAADPHQAMRAAGDEFETFRRT 60
DB 61 FSDLAQLHVTTPGSAOQRFQVSDDELFOGSPNMGSLVAFVFGALCAESVKNKEPPLVG 120
61 FSDLAQLHVTTPGSAOQRFQVSDDELFOGSPNMGSLVAFVFGALCAESVKNKEPPLVG 120
QY 121 QVQEMWVAVLETRLDWHSISGMAEFTLYGDALEEARLRREGNMAVSRTVLTGAVAL 180
121 QVQEMWVAVLETRLDWHSISGMAEFTLYGDALEEARLRREGNMAVSRTVLTGAVAL 180
DB 121 GALVTVGAFPAASK 193
181 GALVTVGAFPAASK 193
QY 181 GALVTVGAFPAASK 193
181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193
181 GALVTVGAFPAASK 193
RESULT 10
AAW97391
ID AAW97391 standard; protein; 193 AA.
XX
AC AAW97391;
XX
DT 20-MAY-1999 (first entry)
XX
DE The rat bcl-2 protein.
XX
XX Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;
KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM multiple sclerosis; myocardial infarction; vitally induced cell death;
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM premature cell death; cell death stimulator; prolonged cell life span;
KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Rattus sp.
XX
XX US5883229-A.
XX
XX 16-MAR-1999.
XX
XX 25-NOV-1997; 97US-00978523.

XX 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX MPI; 1999-214150/18.
XX N-PSDB; AAX15945.
DR
XX Novel bcl-2 homologue of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
XX Disclosure; Col 15-18; 26pp; English.
XX
XX The present sequence represents rat bcl-2 protein (Rbcl-2). The
CC specification also describes human bcl-2 protein (Hbcl-2). Rbcl-2 and
CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-2 and
CC Hbcl-2 may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 193 AA;
Query Match 98.9%; Score 996; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.3e-101;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASAPTRALVADPFGVYKLRQKGYVCGAGPESGPAADPHQAMRAAGDEFETFRRT 60
1 MATPASPTDTRALVADPFGVYKLRQKGYVCGAGPESGPAADPHQAMRAAGDEFETFRRT 60
DB 61 FSDLAQLHVTTPGSAOQRFQVSDDELFOGSPNMGSLVAFVFGALCAESVKNKEPPLVG 120
61 FSDLAQLHVTTPGSAOQRFQVSDDELFOGSPNMGSLVAFVFGALCAESVKNKEPPLVG 120
QY 61 FSDLAQLHVTTPGSAOQRFQVSDDELFOGSPNMGSLVAFVFGALCAESVKNKEPPLVG 120
61 FSDLAQLHVTTPGSAOQRFQVSDDELFOGSPNMGSLVAFVFGALCAESVKNKEPPLVG 120
DB 61 FSDLAQLHVTTPGSAOQRFQVSDDELFOGSPNMGSLVAFVFGALCAESVKNKEPPLVG 120
61 FSDLAQLHVTTPGSAOQRFQVSDDELFOGSPNMGSLVAFVFGALCAESVKNKEPPLVG 120
QY 121 QVQEMWVAVLETRLDWHSISGMAEFTLYGDALEEARLRREGNMAVSRTVLTGAVAL 180
121 QVQEMWVAVLETRLDWHSISGMAEFTLYGDALEEARLRREGNMAVSRTVLTGAVAL 180
DB 121 GALVTVGAFPAASK 193
181 GALVTVGAFPAASK 193
QY 181 GALVTVGAFPAASK 193
181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193
181 GALVTVGAFPAASK 193
RESULT 11
AAW97393
ID AAW97393 standard; protein; 192 AA.
XX
AC AAW97393;
XX
DT 20-MAY-1999 (first entry)
XX
DE Protein sequence of the specification.
XX
XX Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;
KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM multiple sclerosis; myocardial infarction; vitally induced cell death;
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;

KM premature cell death; cell death stimulator; prolonged cell life span;
 KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 OS Unidentified.
 XX
 XX US5883229-A.
 XX
 XX 16-MAR-1999.
 PD
 XX 25-NOV-1997; 97US-00978523.
 PF
 XX 23-FEB-1996; 96US-0012201P.
 PR 11-FEB-1997; 97US-00798897.
 XX
 XX (COCE-) COCENSYS INC.
 PA
 XX Guastella J;
 PI
 XX WPI; 1999-214150/18.
 DR
 XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
 PT modulating programmed cell death.
 PT
 XX
 PS Disclosure; Col 19-20; 26pp; English.
 XX
 CC The specification describes rat bcl-y protein (rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis- conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent. They
 CC may also be used in this way to develop cell lines which remain viable in
 CC culture for an extended period. In contrast, if they act as cell death
 CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites
 CC
 XX
 SQ Sequence 192 AA;
 Query Match 98.4%; Score 991; DB 2; Length 192;
 Best Local Similarity 98.4%; Pred. No. 8.1e-101;
 Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ATPASAPDPRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAARAGDEFTFRRT 61
 DB 1 ATPASAPDPRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAARAGDEFTFRRT 60
 QY 62 SDLAAGLHTVPGSAQGRFTQVSDDELFOGGPNNGRLVAFVFGAALCAESVNMKEPELVG 121
 DB 61 SDLAAGLHTVPGSAQGRFTQVSDDELFOGGPNNGRLVAFVFGAALCAESVNMKEPELVG 120
 QY 122 VDEWVAIVYETRLADVIHSSGGMAEFTALYDGALEEARLRBGNWASRYTLTGAVALG 181
 DB 121 VDDWVAIVYETRLADVIHSSGGMAEFTALYDGALEEARLRBGNWASRYTLTGAVALG 180
 QY 182 ALVTVGAFPAASK 193
 DB 181 ALVTVGAFPAASK 192
 RESULT 12
 ID AAY05533
 AC AAY05533; standard; protein; 192 AA.
 XX
 XX
 DT 05-JUL-1999 (first entry)

XX
 DE Mouse Bcl-w protein derivative.
 XX
 XX Spermatoogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 XX animal model.
 XX
 OS Mus sp.
 XX
 XX M09913710-A1.
 XX
 XX 25-MAR-1999.
 PD
 XX 16-SEP-1998; 98WO-AU000764.
 PF
 XX 16-SEP-1997; 97AU-00009228.
 PR
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA
 XX Cory S, Adams J, Print C, Gibson L, Koentgen F;
 PI
 XX WPI; 1999-243890/20.
 DR
 XX N-PSDB; AAX25135.
 XX
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PT
 XX
 PS Disclosure; Page 39; 52pp; English.
 XX
 CC The present sequence is described of a derivative of mouse Bcl-w (see
 CC also AAY05533), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The derivative
 CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation in at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 CC
 XX
 SQ Sequence 192 AA;
 Query Match 95.2%; Score 958.5; DB 2; Length 192;
 Best Local Similarity 94.8%; Pred. No. 3.1e-97;
 Matches 183; Conservative 6; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MATPASAPDPRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAARAGDEFTFRRT 60
 DB 1 MPTPASAPDPRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAARAGDEFTFRRT 60
 QY 61 FSDLAAGLHTVPGSAQGRFTQVSDDELFOGGPNNGRLVAFVFGAALCAESVNMKEPELVG 120
 DB 61 FSDLAAGLHTVPGSAQGRFTQVSDDELFOGGPNNGRLVAFVFGAALCAESVNMKEPELVG 120
 QY 121 QVDEWVAIVYETRLADVIHSSGGMAEFTALYDGALEEARLRBGNWASRYTLTGAVAL 180
 DB 121 QVQDMIVYVYETRLADVIHSSGGMAEFTALYDGALEEARLRBGNWASRYTLTGAVAL 179
 QY 181 GALVTVGAFPAASK 193
 DB 180 GALVTVGAFPAASK 192
 RESULT 13
 ID AAW36048
 AC AAW36048; standard; protein; 168 AA.
 XX
 XX
 DT AAW36048;

XX Homo sapiens.
OS
XX
PN MO9831800-A2.
XX
PD 23-JUL-1998.
XX
PE 21-JAN-1998; 98MO-US000960.
XX
PR 21-JAN-1997; 97US-0034204P.
PR 21-JAN-1997; 97US-0034205P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
XX
PI Ni J, Rosen CA, Gentz RL, Feng P, Kirsanssen GW, Su JY;
XX
DR WPI; 1998-414099/35.
DR N-PSDB; AAV41925.
XX
PT New isolated polynucleotides and encoded polypeptides - used to develop
PT products for treating e.g. inflammatory diseases, infections,
PT immunological disorders, autoimmune diseases, allergies or tumours.
XX
PS Claim 1; Fig 12A-12D; 120pp; English.
XX
CC This is the amino acid sequence of the cDNA clone Bcl-1ike (HAICH29),
CC used in the method of the invention. The products of the clone can be
CC used for treating conditions associated with abnormal expression of the
CC polypeptides. They can be used for e.g. treating chronic inflammatory
CC diseases, immunological disorders, autoimmune diseases, inflammatory
CC diseases, various allergies, and as anti-infectious agents. The products
CC can also be used for detection and diagnosis
XX
SQ Sequence 365 AA;
Query Match 76.1%; Score 766; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATPASAPDTRALVADPVGKYLKQKGYVCAGPBGSPADPLHQMRAAGDEFFETRRRT 60
DB 1 MATPASAPDTRALVADPVGKYLKQKGYVCAGPBGSPADPLHQMRAAGDEFFETRRRT 60
QY 61 FSDLAAGLHVTGPSAQORFTQVSDELFOGGPNWGRIVAFVFGALCAESVNKEMEPLVG 120
DB 61 FSDLAAGLHVTGPSAQORFTQVSDELFOGGPNWGRIVAFVFGALCAESVNKEMEPLVG 120
QY 121 QVOEMWVAVLETRLADWIHSSGM 144
DB 121 QVOEMWVAVLETRLADWIHSSGM 144

Search completed: March 25, 2004, 15:42:28
Job time : 52 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:18:04 ; Search time 2267.1 Seconds

(without alignment)
7652.923 Million cell updates/sec

Title: US-09-155-327G-8

Perfect score: 581

Sequence: 1 atgcgcagccccagcctcaac.....gccttttgcagcaagtg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560.2	96.4	582	29	AY421022 Mus muscu
2	560.2	96.4	1949	11	AK015644 Mus muscu
3	560.2	96.4	3487	11	AK004680 Mus muscu
4	558.6	96.1	969	13	BY715200 BY715200

5	503.6	86.7	967	13	BU503850	BU503850 AGENCOURT
6	501	86.2	582	29	AY421020	AY421020 Homo sapi
7	477.6	82.2	804	9	AL157542	AL157542 DKFZP761D
8	477	82.1	1030	10	BE793530	BE793530 601590016
9	429	72.6	815	10	BF785386	BF785386 602111728
10	421.8	72.6	854	11	AK013244	AK013244 Mus muscu
11	413	70.4	697	12	B1770566	B1770566 603060362
12	409	70.4	792	12	BG298789	BG298789 602396527
13	407.4	70.1	633	14	CB578463	CB578463 AMGNNUC:N
14	403.6	69.5	530	10	AM258810	AM258810 UMT4a02.Y
15	382.2	65.8	626	14	CA931923	CA931923 CS20C09.Y
16	357.2	61.5	643	12	B1910270	B1910270 603069493
17	353.6	60.9	440	14	CB749817	CB749817 AMGNNUC:M
18	348.4	60.0	559	13	BY704881	BY704881 BY704881
19	339	58.3	437	14	CB790932	CB790932 AMGNNUC:N
20	335.6	57.8	358	14	CF533813	CF533813 UI-M-F10-
21	323.8	55.7	645	13	BY740551	BY740551 BY740551
22	321.8	55.4	362	9	AA569919	AA569919 VO21F08.X
23	321.8	55.4	869	13	BU557268	BU557268 AGENCOURT
24	321.8	55.4	872	13	BU557410	BU557410 AGENCOURT
25	317.4	54.6	548	14	CA407899	CA407899 1004048.H
26	303.2	52.2	460	13	BY285647	BY285647 BY285647
27	302	52.0	410	14	CB804140	CB804140 AMGNNUC:M
28	298	51.3	449	13	BY253191	BY253191 BY253191
29	283.8	48.8	1053	13	BU931540	BU931540 AGENCOURT
30	282	48.5	758	12	B1764428	B1764428 603050701
31	281.4	48.4	327	29	AY421021	AY421021 Pan trogl
32	272.6	46.9	457	10	BB856021	BB856021 BB856021
33	268.6	46.2	430	14	CB760687	CB760687 AMGNNUC:N
34	265.2	45.6	425	13	BY251598	BY251598 BY251598
35	262.2	45.1	467	13	BY253189	BY253189 BY253189
36	261.6	45.0	302	13	BY556166	BY556166 BY556166
37	259	44.6	305	13	BY356183	BY356183 BY356183
38	249.4	42.9	749	12	BG677345	BG677345 602624059
39	241.6	41.6	375	13	BY302913	BY302913 BY302913
40	241	41.5	1064	13	BQ646339	BQ646339 AGENCOURT
41	240	41.3	314	13	BY356000	BY356000 BY356000
42	239.6	41.2	353	13	BY312773	BY312773 BY312773
43	239.6	41.2	372	13	BY133304	BY133304 BY133304
44	239.4	41.2	601	10	BP204905	BP204905 601866718
45	238.8	41.1	452	14	CB786193	CB786193 AMGNNUC:N

ALIGNMENTS

RESULT 1
AY421022 582 bp DNA linear GSS 17-DEC-2003
LOCUS Mus musculus BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence.
DEFINITION Genomic survey sequence.
ACCESSION AY421022 GI:39776973
VERSION AY421022.1 GI:39776973
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 582)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.C., Adams,M.D. and Cargill,M.
TITLE Inferring neutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 582)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.C., Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
 FEATURES Location/Qualifiers
 source 1..582
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1..>582
 /gene="Bcl2l2"
 /locus_tag="Hcm7418"
 ORIGIN
 Query Match 96.4%; Score 560.2; DB 29; Length 582;
 Best Local Similarity 97.8%; Pred. No. 2.8e-132;
 Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1 ATGCCGACCCAGCCTTCAACCCAGACACACGCGCTTCTAGTGTCTTGTAGGCTAT 60
 Db 1 ATGCCGACCCAGCCTTCAACCCAGACACACGCGCTTCTAGTGTCTTGTAGGCTAT 60
 QY 61 AGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGGCTGGGAGAGCCGACGCGCAGC 120
 Db 61 AGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGGCTGGGAGAGCCGACGCGCAGC 120
 QY 121 CCGGTGACCAAGCATGCGGGCTGTGAGAGCAGATTGAGACCCGTTTCGCGCGCAC 180
 Db 121 CCGGTGACCAAGCATGCGGGCTGTGAGAGCAGATTGAGACCCGTTTCGCGCGCAC 180
 QY 181 TTCTCTGACCTGGCCGCTCAGTACAGTGACGCCAGGCTCAGCCAGACAGCTTACAC 240
 Db 181 TTCTCTGACCTGGCCGCTCAGTACAGTGACGCCAGGCTCAGCCAGACAGCTTACAC 240
 QY 241 CAGGTTCCGACGAATCTTTCACAGGGGGCCCTAAGCTGGGGCGCTGTGGGATCTTT 300
 Db 241 CAGGTTCCGACGAATCTTTCACAGGGGGCCCTAAGCTGGGGCGCTGTGGGATCTTT 300
 QY 301 GTCTTTGGGGCTGCGCTGTGAGCTGAGAGTGTCAACAAAGATGAGCCCTTGTGGGA 360
 Db 301 GTCTTTGGGGCTGCGCTGTGAGCTGAGAGTGTCAACAAAGATGAGCCCTTGTGGGA 360
 QY 361 CAAATCCAGATTGATCTGTGCTTACCTTGAAGCAAGTGTGCTGATGATCCACAGC 420
 Db 361 CAAATCCAGATTGATCTGTGCTTACCTTGAAGCAAGTGTGCTGATGATCCACAGC 420
 QY 421 AGTGGCGGCTGGGGGAGCTTCAAGCTCTTATACGGGAGCGGGCCCTGTGAGAGCAGC 480
 Db 421 AGTGGCGGCTGGGGGAGCTTCAAGCTCTTATACGGGAGCGGGCCCTGTGAGAGCAGC 480
 QY 481 CGTCTGGGGAGGAGCACTGGGATGAGTACAGCAATGTGTACGGGGCCGTTGGGACAG 540
 Db 481 CGTCTGGGGAGGAGCACTGGGATGAGTACAGCAATGTGTACGGGGCCGTTGGGACAG 540
 QY 541 GGCGGCTGGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581
 Db 541 GGCGGCTGGTAACTGTAGGGGCTTTTGTCTAGCAAGTG 581
 RESULT 2
 LOCUS AK015644 1949 bp mRNA linear HTC 20-SEP-2003
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493048B08 product:Bcl2-1-like 2, full insert sequence.
 ACCESSION AK015644
 VERSION AK015644.1 GI:12854052
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE
 1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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FEATURES
Source

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/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="MGI:1897773"
/db_xref="taxon:10090"
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/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
132..713
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(MGD|GI:108052)
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/codon_start=1
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/db_xref="GI:12854053"
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AMRAGDEFTFRFTSDLAQLHTVPGSAQORPTQVDELFGGPRWVUAFYF
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RLREGNMAVSRTVLTGAVAGLVGAFPAK"

ORIGIN

Query Match 96.4%; Score 560.2; DB 11; Length 1949;
Best Local Similarity 97.8%; Pred. No. 4,7e-132;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

1 ATGCCGACCCCGCTGACACCCGACACAGCGGCTAGTGGCTGAGCTTTGTAGCTAT 60
132 ATGGCGACCCCGCTGACACCCGACACAGCGGCTAGTGGCTGAGCTTTGTAGCTAT 191
61 AGGCTGAGGACAGAGGATATGCTGTGGAGCTGGGCGCTGGAGAGCCCGCCGAC 120
192 AAGCTGAGGACAGAGGATATGCTGTGGAGCTGGGCGCTGGAGAGCCCGCCGAC 251
121 CGGCTGACCAAGCCATGCGGCGCTGTGGAGACGAGTTGAGACCCGCTTTCCGCGCAC 180
252 CGGCTGACCAAGCCATGCGGCGCTGTGGAGACGAGTTGAGACCCGCTTTCCGCGCAC 311
181 TTCTCTGACCTGGCGCTCAGCTACGACGACCCCGACGGTCCGCCAGCAGCTTACC 240
312 TTCTCTGACCTGGCGCTCAGCTACGACGACCCCGACGGTCCGCCAGCAGCTTACC 371
241 CAGGTTCCGAGGAACTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCTTCTT 300
372 CAGGTTCCGAGGAACTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCTTCTT 431
301 GTCTTTGGGCGCTGCTGTGCTGAGAGTGTCAACAAAGAAATGAGCTTTGGTGGGA 360
432 GTCTTTGGGCGCTGCTGTGCTGAGAGTGTCAACAAAGAAATGAGCTTTGGTGGGA 491
492 CAAATGCAAGATTTGATGTGGCTTACGAGACACGCTGCTGACGATGATCCACAGC 551
361 CAAATGCAAGATTTGATGTGGCTTACGAGACACGCTGCTGACGATGATCCACAGC 420
421 AGTGGGCGCTGGGCGCTTACAGCTCTATACGGGGAAGGGGCGCTTGGAGAGCCACGG 480
552 AGTGGGCGCTGGGCGCTTACAGCTCTATACGGGGAAGGGGCGCTTGGAGAGCCACGG 611
481 CGGCTGCGGAGGCGCACTGGGCGATGAGAGACAGTGGTACGCGGCGCTGGCACATG 540
612 CGGCTGCGGAGGCGCACTGGGCGATGAGAGACAGTGGTACGCGGCGCTGGCACATG 671
541 GGGGCGCTGTAAGTGTAGAGGGGCTTTTGTGACCAAGTG 581
672 GGGGCGCTGTAAGTGTAGAGGGGCTTTTGTGACCAAGTG 712

RESULT 3

AK004680
LOCUS
DEFINITION

AK004680 3487 bp mRNA linear HTC 20-SRP-2003
Mus musculus adult male lung cDNA, RIKEN full-length enriched
library, clone:1200009L24 product:Bcl2-like 2, full insert
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK004680.1 GI:12836027
HTC, CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishide, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

6 (Bases 1 to 3487)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
Direct Submissions

Submitted (10-JUL-2000) Yoshitake Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.

Db	Accession	Version	Source	Organism	Reference Authors	Title	Journal	PubMed	Authors	Comment	Features	Source
Db	190	AA021020	GenBank	Human								
Db	121	AA021020	GenBank	Human								
Db	250	AA021020	GenBank	Human								
Db	181	AA021020	GenBank	Human								
Db	310	AA021020	GenBank	Human								
Db	241	AA021020	GenBank	Human								
Db	370	AA021020	GenBank	Human								
Db	430	AA021020	GenBank	Human								
Db	490	AA021020	GenBank	Human								
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Db	190	AA021020	GenBank	Human								
Db	121	AA021020	GenBank	Human								

[illegible]

German Genome Project.
No SI sequence available.

This clone (DKFZP761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Source
1. 804
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP761D0816"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="761 (synonym: hamy2)"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 82.2%; Score 477.6; DB 9; Length 804;
Best Local Similarity 91.0%; Pred. No. 4,1e-111;
Matches 529; Conservative 0; Mismatches 50; Indels 2; Gaps 2;

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QY 1 ATGCCGACCCGAGCCTCAACCCGAGACACACGCGCTAGTGGCTGACTTTGTAGGCTAT 60
DB 134 ATGCGACCCGAGCCTCGGCCCCGAGACACACGCGCTGCTGTGGACACTTGTAGGCTAT 193
QY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGCCAGCCGCGAC 120
DB 134 AAGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGCCAGACCTGAC 253
QY 121 CGGCTGACCAAGCCATGCGGGCTGCTGGAAGACGATTGAGACCCGTTCCGCGCAC 180
DB 254 CGGCTGACCAAGCCATGCGGGCTGCTGGAAGATGATTGAGACCCGTTCCGCGCAC 313
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DB 314 TTCTCTGACCTGGCCGCTCAGCTCAGTGAACCCAGCTCAAGCCAGAACGCTTCACC 373
QY 241 CAGGTTCCGAGCAATTTTCCAGAGGGGCCCCCTAATCTGGGCGGCTGTGAGCAATCTTT 300
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QY 301 GTCTTTGGGGCTGCCCCCTGTGCTGAGAGTGTCAACAAAGATGAGACCTTTTGTGGA 360
DB 434 GTCTTTGGGGCTGCCCCCTGTGCTGAGAGTGTCAACAAAGATGAGACCTTTTGTGGA 493
QY 351 CAAGTCCAGATTGATGATGCTGAGCTTACCTGAGACACGCTGAGCTGATCCACAGC 420
DB 494 CAAGTCCAGATTGATGATGCTGAGCTTACCTGAGACACGCTGAGCTGATCCACAGC 553
QY 421 AGTGGCGGCTGGGCGGCACTTACAGACTCTATACGGGGAACGGGCGCTTGGAGAGCAG 480
DB 554 AGTGGCGGCTGGGCGGCACTTACAGACTCTATACGGGGAACGGGCGCTTGGAGAGCAG 612
QY 481 CGTTCGCGGAGGAGCACTGGGCGATGATGAGACAGAGTGTGACGGGCGGCTGAGCACTG 540
DB 613 CGTTCGCGGAGGAGCACTGGGCGATGATGAGACAGAGTGTGACGGGCGGCTGAGCACT 671
QY 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGTAGCAAGTG 581
DB 672 GGGGCGCTGTAACTGTAGGGGCTTTTGTGTAGCAAGTG 712
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RESULT 8
LOCUS BE793530
DEFINITION 601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
MRNA sequence.
ACCESSION BE793530
VERSION BE793530.1 GI:10214832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1030)
NIH-MGC <http://mgs.nci.nih.gov/>.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW800 row: P column: 04
High quality sequence start: 5
High quality sequence stop: 709.

FEATURES

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Location/Qualifiers

/organism="Homo sapiens"
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/clone="IMAGE:3944307"
/tissue_type="small cell carcinoma"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG (G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 82.1%; Score 477; DB 10; Length 1030;
Best Local Similarity 88.8%; Pred. No. 6,5e-111;
Matches 516; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCGAGCCTCAACCCGAGACACACGCGCTGATGAGCTTTGTAGGCTAT 60
DB 144 ATGCGACCCGAGCCTCGGCCCCGAGACACACGCGCTGCTGTGAGCAATTTGTAGGCTAT 203
QY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGCCAGCCGCGAC 120
DB 204 AAGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGCCAGACCTGAC 263
QY 121 CGGCTGACCAAGCCATGCGGGCTGCTGGAAGACGATTGAGACCCGTTCCGCGCAC 180
DB 264 CCACTGACCAAGCCATGCGGGCTGCTGGAAGATGATTGAGACCCGCTTCGCGGAC 323
QY 181 TTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGACAGCTTCACC 240
DB 324 TTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGACAGCTTCACC 383
QY 301 GTCTTTGGGGCTGCCCCCTGTGCTGAGAGTGTCAACAAAGATGAGACCTTTTGTGGA 360
DB 444 GTCTTTGGGGCTGCCCCCTGTGCTGAGAGTGTCAACAAAGATGAGACCTTTTGTGGA 503
QY 361 CAAGTCCAGATTGATGATGCTGAGCTTACCTGAGACACGCTGAGCTGATCCACAGC 420
DB 504 CAAGTCCAGATTGATGATGCTGAGCTTACCTGAGACACGCTGAGCTGATCCACAGC 563
QY 421 AGTGGCGGCTGGGCGGCACTTACAGACTCTATACGGGGAACGGGCGCTTGGAGAGCAGCAG 480
DB 564 AGTGGCGGCTGGGCGGCACTTACAGACTCTATACGGGGAACGGGCGCTTGGAGAGCAGCAG 623
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QY 481 CGTCTGGGAGGCACTGGGAGTGTAGACAGTGTGACGCGGGCCGTGGCACTG 540
 DB 624 CCTCTGGCGGGAGGAGGAGTGGGAGTGTAGACAGTGTGACGCGGGCCGTGGCACTG 683
 QY 541 GGGGCGGCTGTACTGTAGGGGCTTTTGTGTAGCAAGT 581
 DB 684 GGGGCGGCTGTACTGTAGGGGCTTTTGTGTAGCAAGT 724

RESULT 9
 LOCUS BF785386 815 bp mRNA linear EST 12-JAN-2001
 DEFINITION 60211728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
 5', mRNA sequence.
 ACCESSION BF785386
 VERSION BF785386.1 GI:12090422
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 815)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHM9853 row: h column: 07
 High quality sequence start: 3
 High quality sequence stop: 650.
 Location/Qualifiers
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 /clone_lib="NCI_CGAP_Kid14"
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 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library. |"

ORIGIN
 Query Match 73.8%; Score 429; DB 10; Length 815;
 Best Local Similarity 94.7%; Pred. No. 1,1e-98;
 Matches 520; Conservative 0; Mismatches 20; Indels 9; Gaps 7;

QY 21 CCCAGACACACGGCTCTAGTGTGCTGACTTGTAGCTTAGGCTGAGGACAGAGGTTA 80
 DB 2 CCCAGACACACGGCTCTAGTGTGCTGACTTGTAGCTTAGGCTGAGGACAGAGGTTA 60
 QY 81 TGTCTGTGAGCTGGGCTGGGAGAGCCCGCCGACCGGCTGACCAAGCATGG 140
 DB 61 TGTCTGTGAGCTGGGCTGGGAGAGCCCGCCGACCGGCTGACCAAGCATGG 120
 QY 141 GGCTGTGAGAGCAAGTTGAGACCCGCTTCGCGGCACTTCTGTGACCTGCGGCTCA 200
 DB 121 GGCTGTGAGAGCAAGTTGAGACCCGCTTCGCGGCACTTCTGTGACCTGCGGCTCA 179
 QY 201 GCTACAGTGAACCCGAGGCTCAGCCAGCAAGCTTACCAAGTTTCGAGCAATTTT 260
 DB 180 GCTACAGTGAACCCGAGGCTCAGCCAGCAAGCTTACCAAGTTTCGAGCAATTTT 239
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 DB 533 GGCTTTT 541

RESULT 10
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 DEFINITION AK013244 854 bp mRNA linear HTC 20-SHP-2003
 Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
 enriched library, clone:2810435k13 Product:Bcl2-1-like 2, full insert
 sequence.
 ACCESSION AK013244
 VERSION AK013244.1 GI:12850487
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Komno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Harada, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multiplexed capillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 JOURNAL 5
 REFERENCE
 AUTHORS
 TITLE
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation

JOURNAL
REFERENCE
AUTHORS
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 854)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furukoshi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hirakawa, T., Hori, P., Imotani, K., Ishi, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawal, J., Kojima, Y., Kono, H., Kouda, M.,
Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tajima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL
Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5'-GAGGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using triazole thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to R0 = 7.5 and subtraction to
R0 = 37.5. Second strand cDNA was prepared with the primer adapter
of sequence [5'-
GAGGAGAGATCTCGAGTTAATTAAATATATCCCCCCCCCCC 3']. cDNA was cleaved
with XhoI and SfiI. Cloning sites, 5' end: XhoI; 3' end: SfiI.
Host: SOLR.

FEATURES
source
Location/Qualifiers

1..854
/organism="Mus musculus"
/mol_type="cDNA"
/strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="2810435A13"
/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10, 11 days embryo"
196..732
/note="unlabeled protein product; Bcl2-like 2
(MGI:MGI:108052)
putative"
/codon_start=1
/protein_id="BAB28740.1"
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LHGKIGPLMGWCAGRG"

ORIGIN

Query Match 72.6%; Score 421.8; DB 11; Length 854;
Best local similarity 98.4%; Pred. No. 7.6e-97;
Matches 426; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

DB 1 ATGGCGACCCCGAGCTCAACCCGAGACACACGCGCTGTAGTGGCTGACTTTGTAGGCTAT 60
DB 196 ATGGCGACCCCGAGCTCAACCCGAGACACACGCGCTGTAGTGGCTGACTTTGTAGGCTAT 255
DB 61 AGGCTAGGCGACGAGGCTTATGTGTGAGCTGGGCTGGGGAAGGCCCGCCCGAC 120

DB 256 AACCTAGGCGACGAGGCTTATGTGTGAGCTGGGCTGGGGAAGGCCCGCCCGAC 315
DB 121 CCGCTGACCAAGCATGAGGCGCTGCTGAGACGAGTTGAGACCCGTTCCGCGAC 180
DB 316 CCGCTGACCAAGCATGAGGCGCTGCTGAGACGAGTTGAGACCCGTTCCGCGAC 375
DB 181 TTCTGACCTGCGCTGAGTACGTAACGTAACCCGAGCTGAGCCAGCAAGCTTCA 240
DB 376 TTCTGACCTGCGCTGAGTACGTAACGTAACCCGAGCTGAGCCAGCAAGCTTCA 435
DB 241 CAGGTTCCGAGCACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGGCACTTCTT 300
DB 436 CAGGTTCCGAGCACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGGCACTTCTT 495
DB 301 GTCTTGGGCGCTGCTGCTGAGTACGTAACCAAGAAAGAGCCCTTGGTGGGA 360
DB 496 GTCTTGGGCGCTGCTGCTGAGTACGTAACCAAGAAAGAGCCCTTGGTGGGA 555
DB 361 CAAGTCCAGATTTGATGCTGAGCTTCTGAGACACGCTGCTGAGTCAAGC 420
DB 556 CAAGTCCAGATTTGATGCTGAGCTTCTGAGACACGCTGCTGAGTCAAGC 615
DB 421 AGTGGCGCTGGG 433
DB 616 AGTGGCGCTGGG 628

RESULT 11
LOCUS B1770566
DEFINITION 603060362P1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:520962 5',
mRNA sequence.
ACCESSION B1770566
VERSION B1770566.1 GI:15762144
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue procurement: nih.gov

cDNA library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: L1M1526 row: K column: 15
High quality sequence start: 21
High quality sequence stop: 695.
Location/Qualifiers

FEATURES
source

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/db_xref="taxon:9606"
/clone="IMAGE:520962"
/lab_host="DH10B"
/clone_lib="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source:
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026 Note:

ORIGIN this is a NIH_MGC Library."

Query Match 71.1%; Score 413; DB 12; Length 697;
Best Local Similarity 90.1%; Pred. No. 1.2e-94;
Matches 498; Conservative 0; Mismatches 50; Indels 5; Gaps 5;

QY 1 ATGCCGACCCAGCTCAACCCAGACACACGCGCTCTAGTGGCTGATTTGATGCTAT 60
DB 145 ATGGGACCCAGCTCGGCCCCAGACACACGCGCTCTAGTGGCTGATTTGATGCTAT 204
QY 61 AGGCTGAGGACGAGAGGTTATGCTGTGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120
DB 205 AAGCTGAGGACGAGAGGTTATGCTGTGAGCTGGGCTGGGAGAGGCCAGCTGAC 264
QY 121 CCGCTGACACGAGCTATGCGGGCTGCTGAGACGAGTTTGAGACCTTTTCGCGCAC 180
DB 265 CCGCTGACACGAGCTATGCGGGCTGAGAGATGATTCGAGACCTTCGCGCAC 324
QY 181 TTCTGTACCTGGGCGCTCAGCTACAGTGAAGCCAGGCTCAGGCGCAGACGCTTAC 240
DB 325 TTCTGTATCTGGCGGCTCAGCTGATGATGACCCAGCTCAGCCAGACGCTTAC 384
QY 241 CAGGTTTCCGACGAACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTTGAGCTTCTT 300
DB 385 CAGGCTCCGATGAACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTTGAGCTTCTT 444
QY 301 GTCTTTGGGGCTGCCCTGTG- TGCTGAGAGTGTCAACAGAAATGAGACCTTTGAG 359
DB 445 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGAGAACCACTGTGG 504
QY 360 ACAAGTCCAGAGTTGATGATCGTGGCTTACT- GAGACACGCTGTGCTGATGATCCACA 418
DB 505 ACAAGTGAAGAGTGAAGTGTGCTTACTGAGAGACGCGGCTGCTGATGATCCACA 564
QY 419 GCAGTGGGCGGCTGGGCGGACTTCAAGCTCTATAC- GGGGAGCGGGGCGCTTGGAGAGCA 477
DB 565 GCAGTGGGCGGCTGGGCGGAGTTACAGCTCTATACGGGGGAGCGGGGCGCTTGGAGAGAG 624
QY 478 CGGCGTCTGCGGAGGAGGCACTGGGCA- TGAATGAGCAAG- TGGTGAAGGGGCGCTTGG 535
DB 625 CGGCGTCTGCGGAGGAGGCACTGGGCACTGAGTGAAGCAATTCCTGACGAGGAGCCGCTG 684
QY 536 CACTGGGGGCGCT 548
DB 685 CACTGGGGGCGCT 697

RESULT 12
LOCUS BG298789 792 bp mRNA linear EST 21-FEB-2001
DEFINITION 602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:451125 5',
mRNA sequence.
ACCESSION BG298789
VERSION BG298789.1 GI:13063794
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 792)
AUTHORS NIH-MGC <http://nigc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
cgapds-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

FEATURES
source
1..792
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/db_xref="taxon:10090"
/clone="IMAGE:451125"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-Sport6; Site: 1; Note: 1;
Site: 2; Salt: Cloned unidirectionally; oligo-dt primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.4%; Score 409; DB 12; Length 792;
Best Local Similarity 97.5%; Pred. No. 1.4e-93;
Matches 426; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ATGCCGACCCAGCTCAACCCAGACACACGCGCTCTAGTGGCTGATTTGATGCTAT 60
DB 99 ATGGGACCCAGCTCAACCCAGACACACGCGCTCTAGTGGCTGATTTGATGCTAT 158
QY 61 AGGCTGAGGACGAGAGGTTATGCTGTGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120
DB 159 AAGCTGAGGACGAGAGGTTATGCTGTGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 218
QY 121 CCGCTGACACGAGCTATGCGGGCTGCTGAGAGCGAGTTGAGACCGCTTCGCGCAC 180
DB 219 CCGCTGACACGAGCTATGCGGGCTGCTGAGAGCGAGTTGAGACCGCTTCGCGCAC 278
QY 181 TTCTGTACCTGGGCGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGACGCTTAC 240
DB 279 TTCTGTACCTGG- GCTAGCTACAGTGAAGCCAGGCTCAGCCAGACGCTTAC 337
QY 241 CAGGTTTCCGACGAACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTTGAGCTTCTT 300
DB 338 CAGGTTTCCGACGAACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTTGAGCTTCTT 397
QY 301 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAGAAATGAGACCTTTGATGGA 360
DB 398 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAGAAATGAGACCTTTGATGGA 457
QY 361 CAAGTCCAGAGTTGATGATGCTGGCTTACCTGAGACACGCTGGGCTGATGATCCACAG 420
DB 458 CAAGTCCAGAGTTGATGATGCTGGCTTACCTGAGACACGCTGGGCTGATGATCCACAG 517
QY 421 AGTGGCGCTGGGCGGA 437
DB 518 AGTGGCGCTGGGTAGA 534

RESULT 13
LOCUS CB578463 623 bp mRNA linear EST 03-APR-2003
DEFINITION AMGNNUC:NR01-00100-H10-A nr01 (10855) Rattus norvegicus cDNA
clone nr01-00100-h10 5', mRNA sequence.
ACCESSION CB578463
VERSION CB578463.1 GI:29522504
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 623)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick

RESULT 15

CA391923

CA391923 626 bp mRNA linear EST 06-NOV-2002
cs20c09.y1 Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs20c09
5', mRNA sequence.

ACCESSION

CA391923

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Wistow G
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gwaeme@helix.nih.gov
Plate: 20 row: C column: 09
Seg primer: M13RPI reverse primer (ABI).
Location/Qualifiers

FEATURES

1..626

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/mol_type="mRNA"

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/lab_host="EMD10B"

/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs"/note="Organ: Eye; Vector: PCWVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pcwvSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the SuperScript
Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>". The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match

Best Local Similarity

Matches 408; Conservative

65.8%; Score 382.2; DB 14; Length 626;

90.3%; Pred. No. 8.8e-87;

0; Mismatches 44; Indels 0; Gaps 0;

QY

DB

QY

DB

QY

DB

QY

DB

QY

1 ATGCCGACCCAGCCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
175 ATGGCGACCCAGCCTCGGCCCGACACACAGCGCTCTGTGCGACACTTTGTAGGCTAT 224
61 AGGCTGAGGACGAAAGGTTATGTGTGAGCTGAGCTGGGCGGAGGCGGCGCGAC 120
235 AAGCTGAGGACGAAAGGTTATGTGTGAGCTGAGCTGGGCGGAGGCGGCGGAGCTGAC 294
121 CCGCTGCACCAAGCATGCGGGCTGCTGAGACGAGTTTGACCCCGTTTCCGCGGAC 180

DB 295 CCGCTGCACCAAGCATGCGGGCTGCTGAGACGAGTTTGACAGACCCCGTTCCGCGGAC 354
QY 181 TTCTGTGACCTGAGCGGCTCAGCTACACGTGACCCAGGCTGACCCAGCAAGCTTAC 240
DB 355 TTCTGTGACCTGAGCGGCTCAGCTGAGTGTGACCCAGGCTGACCCAGCAAGCTTAC 414
QY 241 CAGGTTTCCGACGAACTTTTCCAGGCGGCGGCTTACTGCGGCGGCTTGTGCAATCTTT 300
DB 415 CAGGTTTCCGACGAACTTTTCCAGGCGGCGGCTTACTGCGGCGGCTTGTGCAATCTTT 474
QY 301 GTCTTTGGGGGCTGCGGCTTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGCGGA 360
DB 475 GTCTTTGGGGGCTGCGGCTTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGCGGA 534
QY 361 CAGGTTTCCGACGAACTTTTCCAGGCGGCGGCTTACTGCGGCGGCTTGTGCAATCTTT 420
DB 535 CAGGTTTCCGACGAACTTTTCCAGGCGGCGGCTTACTGCGGCGGCTTGTGCAATCTTT 594
QY 421 AGTGGCGGCTGCGGCTTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGCGGA 452
DB 595 AGTGGCGGCTGCGGCTTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGCGGA 626

Search completed: March 29, 2004, 07:28:10
Job time : 2269.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:01:08 / Search time 2753.26 Seconds

(without alignments)
9146.355 Million cell updates/sec

Title: US-09-155-327G-8

Perfect score: 581

Sequence: 1 atgcgcaccacagctcaac.....gcttttttctgtagcaagt 581

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_pl:*
8: gb_pr:*
9: gb_px:*
10: gb_ro:*
11: gb_srs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_srs:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rtd:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_sv:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	581	100.0	581	6	AX030819
3	560.2	96.4	582	10	MMT59746
4	560.2	96.4	3476	10	AF030769
5	544.2	93.7	582	10	AF096291
6	544.2	93.7	1110	10	AY185100
7	544.2	93.7	3487	10	AY185098
8	541	93.1	3473	10	AY170344
9	540.6	93.0	579	6	AR020779
10	505.8	87.1	582	6	AX461423
11	505.8	87.1	582	9	HSU59747
12	502.6	86.5	3542	9	D87461
13	501	86.2	583	6	AX022529
14	501	86.2	583	6	AX030817
15	457.4	85.6	579	6	AR020780
16	451.4	77.7	220818	2	AC128940
17	451.4	77.7	223933	2	AC097389
18	421.8	72.6	3815	10	BC040369
19	421.8	72.6	237561	10	AC116591
20	407.4	70.1	210784	2	AC119293
21	407.4	70.1	263901	2	AC115371
22	390.8	67.3	148278	2	AC079885
23	390.8	67.3	180655	2	AC084240
24	390.8	67.3	221557	2	AC134055
25	364.8	62.8	1098	6	AR432565
26	364.8	62.8	1098	6	BD078624
27	364.4	62.7	1864	6	BD191165
28	364.2	62.7	196292	9	CNS0000B
29	315	54.2	505	10	AY185099
30	233.8	40.2	749	5	XLRI
31	212.2	36.5	6049	6	AX345130
32	191	32.9	6049	6	AX345131
33	142.4	24.5	1252	4	AB073983
34	140.8	24.0	1163	4	AB080951
35	139.2	23.8	1184	5	CG026645
36	138.2	23.8	1184	5	CG026645
37	137.6	23.7	541	4	AF245488
38	137.6	23.7	766	4	AF164517
39	136	23.4	541	4	AF245487
40	136	23.4	541	4	AF245489
41	134.6	23.2	636	6	BD097037
42	134.6	23.2	702	6	BD084108
43	134.6	23.2	702	6	BD102202
44	134.6	23.2	702	9	BT007208
45	134.6	23.2	702	12	BT008248

ALIGNMENTS

RESULT 1
AX022531
LOCUS AX022531 581 bp DNA
DEFINITION Sequence 8 from Patent EP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS
SOURCE unidentifed
ORGANISM unidentifed
REFERENCE 1
AUTHORS Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 8 04-AUG-1999;

FEATURES

source
1..581
/organism="unidentified"
/mol_type="unassigned DNA"
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CDS

/note="unnamed protein product"
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/translation="MPTASTPDTALVADPVGRRLRQKGVYCGAPGEPADPLHQ
AMRAAGDEFERFRRTFSDLAQLHTVPSAQOQRTQVSDLEFQSGPMGLVAFV
GAALCAESVYKEMEPVGVQVDMIVAVLETRLADWIHSSGGMADFTALYDGALEDA
RLREGNMA"

ORIGIN

Query Match 100.0%; Score 581; DB 6; Length 581;
Best Local Similarity 100.0%; Pred. No. 6.5e-126;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 AGGCTAGGACGAGAGGATATGCTGTGAGCTGGGCTGGGAGAGGCCGACCCGAC 120
61 AGGCTAGGACGAGAGGATATGCTGTGAGCTGGGCTGGGAGAGGCCGACCCGAC 120
121 CCAGCTCACCAGACGACCTGAGGAGAGGAGTGAAGAGTGAAGAGTGAAGAGTGA 180
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RESULT 2
LOCUS AX030819 581 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 8 from Patent WO9735971.
ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE

1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibbon, L.M.
A novel mammalian gene, bcl-2, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 8 02-OCT-1997
ADAMS JERRY MCKEE (AU) ; HOLMGREN SHARON P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)

FEATURES

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Query Match 100.0%; Score 581; DB 6; Length 581;
Best Local Similarity 100.0%; Pred. No. 6.5e-126;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
LOCUS MM059746 582 bp mRNA linear ROD 29-SEP-1996
DEFINITION Mus musculus Bcl-2 (bcl-2) mRNA, complete cds.

ACCESSION US9746 GI:1572494
 VERSION US9746.1
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 582)
 REFERENCE 1 Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M., and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)
 JOURNAL 96358615
 MEDLINE 8761287
 PUBMED 8761287
 REFERENCE 2 (bases 1 to 582)
 AUTHORS Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and Cory, S.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
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 Best Local Similarity 97.8%; Pred. No. 5e-121;
 Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1 ATCCGACCCAGCCTCAACCCAGACACACCGGCTCTGTGTGCTGACTTTGTAGGCTAT 60
 DB 1 ATGGGACCCAGCCTCAACCCAGACACACCGGCTCTGTGTGCTGACTTTGTAGGCTAT 60
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 DB 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGGCTGGGGAAGCCAGCCGCGAC 120
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 DB 121 CCGCTGACCAACCCAGCCTCAACCCAGACACCGGCTCTGTGTGAGAGCTTTGCGCGAC 180
 QY 181 TTCTCTGACCTGGCCGCTCACTGACACGTAACCCAGGCTCAAGCCAGCAAGCTTTAC 240
 DB 181 TTCTCTGACCTGGCCGCTCACTGACACGTAACCCAGGCTCAAGCCAGCAAGCTTTAC 240
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DB 361 CAAGTCAGGATTGATCGTGGCTTACTGAGACACGCTCTGGCTACTGATCCACAGC 420
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 DB 421 AGTGGGCGCTGGGCGGCACTTCAAGCTCTATACAGGAGACGGGCGCTTGAGAGACGACG 480
 QY 481 CGTCTGCGGAGAGGCAACTGGGCAATGATGAGACAGTGTGAACGGGCGCTTGAGACTG 540
 DB 481 CGTCTGCGGAGAGGCAACTGGGCAATGATGAGACAGTGTGAACGGGCGCTTGAGACTG 540
 QY 541 GGGGCGCTGTACTGAGGCGCTTTTGTGTAAGCAAGTG 581
 DB 541 GGGGCGCTGTACTGAGGCGCTTTTGTGTAAGCAAGTG 581
 RESULT 4
 AF030769 3476 bp mRNA linear ROD 16-NOV-1997
 LOCUS Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
 DEFINITION AF030769
 ACCESSION AF030769
 VERSION AF030769.1 GI:2623249
 KEYWORDS
 ORGANISM Mus musculus (house mouse)
 SOURCE Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3476)
 REFERENCE 1 Ross, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and Macgregor, G.R.
 AUTHORS Bcl-w is required for testis homeostasis
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 3476)
 REFERENCE Ross, A.J. and Macgregor, G.R.
 AUTHORS Direct Submission
 TITLE Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA
 JOURNAL Location/Qualifiers
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ORIGIN

Query Match 96.4%; Score 560.2; DB 10; Length 3476;
 Best Local Similarity 97.8%; Pred. No. 3.8e-121;
 Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCCTCAACCCCAACACACGCGCTCTAGTGTGACTTTGAGCTAT 60
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 QY 61 AGGCTGAGGCAAGGAGTATGCTGTGAGAGCTGGGCTGGGAGAGCCGACCGCGAC 120
 DB 239 AGGCTGAGGCAAGGAGTATGCTGTGAGAGCTGGGCTGGGAGAGCCGACCGCGAC 298
 QY 121 CGGCTGACCAAGCCTATCGGGCTGTGAGAGAGTGTGAGAGCCGCTTCCGCGAC 180
 DB 239 CGGCTGACCAAGCCTATCGGGCTGTGAGAGAGTGTGAGAGCCGCTTCCGCGAC 358
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 DB 479 GTCTTTGGGGCTGCGCTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTTGGGGA 538
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 QY 541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGCTGCAAGTG 581
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RESULT 5
 AF096291 582 bp mRNA linear ROD 28-FEB-2000

LOCUS AF096291 Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.

ACCESSION AF096291

VERSION AF096291.1 GI:3747129

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 582)

AUTHORS Hammer, S., Skogjose, Y. and Lindholm, D.

TITLE Differential expression of bcl-w and bcl-x messenger RNA in the

JOURNAL Neurosciences 91 (2), 673-684 (1999)

MEDLINE 99292146

PUBMED 10366024

REFERENCE 2 (bases 1 to 582)

AUTHORS Hammer, S., Skogjose, Y. and Lindholm, D.

TITLE Direct Submission

JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala

FEATURES Location/Qualifiers

source 1..582

ORIGIN

Query Match 93.7%; Score 544.2; DB 10; Length 582;
 Best Local Similarity 96.0%; Pred. No. 2.9e-117;
 Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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RESULT 6
 AY185100 1110 bp mRNA linear ROD 24-JUN-2003
 LOCUS AY185100 Rattus norvegicus BCL-WB1 mRNA, complete cds.
 DEFINITION AY185100
 ACCESSION AY185100.1 GI:32185284
 KEYWORDS

SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1110)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)

JOURNAL MEDLINE 22672518
PUBMED 12787069

REFERENCE 2 (bases 1 to 1110)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
Submitted (21-NOV-2002) Neurology Research, The Children's Hospital
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers

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929 AGTGGCGGCTGGCGGAGTTTCAAGCTCTTATACGGGGAACGGGCGCTGGAGGACGACGG 988
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Db 989 CGTCTGGCGGAGGGGAACCTGGGCATCAGTAGAGCACTGCTGACGGGGGCTGTGGCACTG 1048

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Db 1049 GGGGCGCTGTGACTGTAGAGGCGCTTTTGTCTGACAGTG 1089

RESULT 7
LOCUS AY185098 3487 bp mRNA linear ROD 24-JUN-2003
DEFINITION Rattus norvegicus BCL-W mRNA, complete cds.
ACCESSION AY185098
VERSION AY185098.1 GI:32185280
KEYWORDS

SOURCE
ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 3487)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)

JOURNAL MEDLINE 22672518
PUBMED 12787069

REFERENCE 2 (bases 1 to 3487)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
Submitted (21-NOV-2002) Neurology Research, The Children's Hospital
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers

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230 AGGCTGAGCGAAGGGTTATGTCTGTGAGCTGGGCTTGGGAAAGCCCGACGCCGAC 289
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290 CGGCTGACCAAGCCATGCGGGGCTGTGAGAGAGATTGAGACCCGTTCCGCGGACCC 349
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	QY	421	AGTGGCCGCTGGGGGAGCACTTCAACAGCTCTAARACGGGGACGGGGGCCCTGGAGAAGCACGCG	480
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LOCUS			Mus musculus Bcl2-like protein 2 mRNA, complete cds.	
DEFINITION			Ay170344	
ACCESSION			Ay170344.2 GI:34857712	
VERSION				
KEYWORDS				
SOURCE			Mus musculus (house mouse)	
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE			1 (bases 1 to 3473)	
AUTHORS			Su,H.-Y.	
TITLE			Extraction from neonatal mouse skin after IGF-I stimulation	
JOURNAL			Unpublished	
REFERENCE			2 (bases 1 to 3473)	
AUTHORS			Su,H.-Y.	
TITLE			Direct Submission	
JOURNAL			Submitted (22-OCT-2002) Biotechnology, Pingtung University, No. 1, Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan	
REFERENCE			3 (bases 1 to 3473)	
AUTHORS			Su,H.-Y.	
TITLE			Direct Submission	
JOURNAL			Submitted (22-SEP-2003) Biotechnology, Pingtung University, No. 1, Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan	
COMMENT			Sequence update by submitter	
REMARK			On Sep 22, 2003 this sequence version replaced gi:27497698.	
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			/dev_stage="neonatal"	
			/note="isolated after IGF-1 stimulation"	
			182..763	
			/note="c98; Bcl2-c98"	
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			/product="Bcl2-like protein 2"	
			/protein_id="AA013177.2"	
			/db_xref="gi:34857713"	
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ORIGIN				
Query Match			93.1%; Score 541; DB 10; Length 3473;	
Nest local Similarity			95.7%; Pred. No. 1,2e-116;	
Matches 556; Conservative			0; Mismatches 25; Indels 0; Gaps 0;	

[illegible]

QY 121 CCGCTGCAACCAAGCCATGCGGCTGTGAGACGAGTTTGAAGCCGTTTCGCGCACC 180
DB 121 CCGCTGCAACCAAGCCATGCGGCTGTGAGACGAGTTTGAAGCCGTTTCGCGCACC 180
QY 181 TTCTGTGACTGCGGCTGCTGAGTACAGTCCAGGCTGACCCAGCAACGCTTACC 240
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DB 301 GTCTTTGGGGCTGCGCTGTGTGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
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DB 421 AGTGGCGGCTGGGCGGACCTTACAGCTTATACGGGACGGGCGCTTGGAGACGAC 480
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DB 481 CGTCTGCGGAGGGGCACTGGGCAATGAGTGTGAGAGACAGTGTGACGGGCGCTGTG 540
QY 541 GGGGCGCTGTGACTGAGGGGCTTTTGTGAGCAAG 579
DB 541 GGGGCGCTGTGACTGAGGGGCTTTTGTGAGCAAG 579

RESULT 10
AX481423 582 bp DNA linear PAT 16-AUG-2002
LOCUS AX481423
DEFINITION Sequence 37 from Patent W002055693.
ACCESSION AX481423
VERSION AX481423.1 GI:22316337
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Kreutzer, R., Limer, S., Roat, S. and Hadwiger, P.
JOURNAL Method for inhibiting the expression of a target gene
REFERENCE Parent: WO 02055693-A 37 18-JUL-2002;
Ridopharma AG (DE)
FEATURES
source
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/organism="Homo sapiens"
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ORIGIN
Query Match 87.1%; Score 505.8; DB 6; Length 582;
Best Local Similarity 91.9%; Pred. No. 3e-108;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 181 TTCTGTGACTGCGGCTGCTGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
DB 181 TTCTGTGACTGCGGCTGCTGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
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DB 241 CAGGTTTCCGAGCACTTTTCAAGGGGGCCCTAATGAGGCGCTTGTGGCAATCTTT 300
QY 301 GTCTTTGGGGCTGCGCTGTGTGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
DB 301 GTCTTTGGGGCTGCGCTGTGTGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
QY 361 CAAGTCCAGGATTTGATGCTGAGCTTACCTGAGACAGCTGCTGATGATCCAGAC 420
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DB 421 AGTGGCGGCTGGGCGGACCTTACAGCTTATACGGGACGGGCGCTTGGAGACGAC 480
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DB 481 CGTCTGCGGAGGGGCACTGGGCAATGAGTGTGAGAGACAGTGTGACGGGCGCTGTG 540
QY 541 GGGGCGCTGTGACTGAGGGGCTTTTGTGAGCAAG 581
DB 541 GGGGCGCTGTGACTGAGGGGCTTTTGTGAGCAAG 581

RESULT 11
HSU59747 582 bp mRNA linear PRI 29-SEP-1996
LOCUS HSU59747
DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59747
VERSION U59747.1 GI:1572492
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.
JOURNAL Oncogene 13 (4), 665-675 (1996)
MEDLINE 8761287
PUBMED 96358615
REFERENCE
AUTHORS Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
Cory, S.
TITLE Direct Submision
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia
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QARAAGDEFETFRFTFSDLAQLHTVGSAAQRTVSDLETFQGFVWGRVLAFFV
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AX022529 583 bp DNA linear PAT 07-SEP-2000
LOCUS AX022529 Sequence 6 from Patent EP0932674.
DEFINITION AX022529
ACCESSION AX022529
VERSION AX022529.1 GI:10046125
KEYWORDS
SOURCE unclassified
ORGANISM unclassified.
REFERENCE
AUTHORS 1
TITLE Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
JOURNAL A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: EP 0932674-A 6 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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Query Match 86.2%; Score 501; DB 6; Length 583;
Best Local Similarity 91.4%; Pred. No. 4e-107;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 1 ATGGCGACCCCAAGCCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGCGAGAGGGTTATGCTGTGAGAGCTGGGCTGGGGAGAGCCGACGCGGAC 120
DB 61 AAGCTGAGGCGAGAGGGTTATGCTGTGAGAGCTGGGCTGGGGAGAGCCGACGCGGAC 120
QY 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGATTGAGACCCGTTCCGCGGAC 180
DB 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGATTGAGACCCGTTCCGCGGAC 180
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QY 541 GGCGCCCTGTGTAAGTGAAGGAGGAGTGTGTAAGGAGTGTG 581

DB 541 GGCGCCCTGTGTAAGTGAAGGAGGAGTGTGTAAGGAGTGTG 581
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LOCUS AX030817 583 bp DNA linear PAT 20-SEP-2000
DEFINITION AX030817 Sequence 6 from Patent WO9735971.
ACCESSION AX030817
VERSION AX030817.1 GI:10278311
KEYWORDS
SOURCE unclassified
ORGANISM unclassified.
REFERENCE
AUTHORS 1
TITLE Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
JOURNAL A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZANNE (AU)
; GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 86.2%; Score 501; DB 6; Length 583;
Best Local Similarity 91.4%; Pred. No. 4e-107;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGCCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 1 ATGGCGACCCCAAGCCTTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGCGAGAGGGTTATGCTGTGAGAGCTGGGCTGGGGAGAGCCGACGCGGAC 120
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DB 121 CCGCTGACCAAGCCATGCGGCTGTGAGAGAGATTGAGACCCGCTTCCGCGGAC 180
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Search completed: March 29, 2004, 06:11:59
Job time : 2757.26 secs

QY 481 CGTCTGCGGAGGAGCACTGGCATGATGAGCAGAGTGTGACGCGGGCCGTTGACACTG 540
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QY 541 GGGGCCCTGTGTAACCTGAGGGGCTTTTGTCTAGCAAGTG 581
Db 541 GGGGCCCTGTGTAACCTGAGGGGCTTTTGTCTAGCAAGTG 581

RESULT 15
AR020780 579 bp DNA linear PAT 05-DEC-1998
LOCUS AR020780
DEFINITION Sequence 2 from patent US 5789201.
ACCESSION AR020780
VERSION AR020780.1 GI:3975395
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 579)
AUTHORS Guastella,J.
TITLE Genes coding for bcl-2 homologues
JOURNAL Patent: US 5789201-A 2 04-AUG-1998;
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Location/Qualifiers
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/mol_type="unassigned DNA"

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Best Local Similarity 91.2%; Pred. No. 2.8e-106;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 1 ATGCCGACCCAGCCTCGGCCAGACACAGGGGCTCTGTGAGAGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTTGGGAAAGGCCCGCCGAC 120
Db 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTTGGGAAAGGCCCGCCGAC 120
QY 121 CCGGTGACCAAGGCAATGCGGGCTGTGAGAGAGATTGAGACCCGTTCCGCGCAC 180
Db 121 CCACTGACCAAGGCAATGCGGGCTGTGAGAGATTGAGACCCGTTCCGCGCAC 180
QY 181 TTCTCTGACCTGGCGGCTACAGTGAACCCAGGCTCAGGCCAGCAAGCTTCACC 240
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QY 241 CAGGTTCCGACGAACTTTTCCAGGGGGCTTAATGCGGCGCTTTGTGCAATCTTT 300
Db 241 CAGGTTCCGACGAACTTTTCCAGGGGGCTTAATGCGGCGCTTTGTGCAATCTTT 300
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QY 361 CAAATCCAGAGATTGATGATGAGCTTACCTGAGAGACAGTGTGAGCTGATCCAGC 420
Db 361 CAAATGAGAGATGATGATGAGCTTACCTGAGAGACAGTGTGAGCTGATCCAGC 420
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QY 481 CGTCTGCGGAGGAGCACTGGCATGATGAGCAGAGTGTGACGCGGGCCGTTGGCACTG 540
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QY 541 GGGGCCCTGTGTAACCTGAGGGGCTTTTGTCTAGCAAG 579
Db 541 GGGGCCCTGTGTAACCTGAGGGGCTTTTGTCTAGCAAG 579

GenCore version 5.1.6
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneeqn20058:*
9: geneeqn20068:*
10: geneeqn20078:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	544.2	93.7	582	9	ADB52996
5	540.6	93.0	579	2	AAV28333
6	540.6	93.0	579	2	AAV28333
7	505.8	87.1	582	6	ABV78153
8	505.8	87.1	582	6	ABV78153
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10	505.8	87.1	582	6	ABX09972
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16	497.4	85.6	579	2	AAV28334
17	364.8	62.8	1098	2	AAV41825
18	364.4	62.7	1864	6	AAV59630
19	364.4	62.7	1864	6	AAV59630
20	364.4	62.7	1864	6	ACD82760
21	212.2	36.5	6049	6	AB132228
22	191	32.9	6049	6	AB132229
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27	137.8	23.7	150	4	ABA32370
28	137.8	23.7	150	4	AAK39424
29	137.8	23.7	150	4	AAK39424
30	137.8	23.7	150	4	ABK39016
31	137.8	23.7	150	5	AAI05940
32	137.8	23.7	150	5	ABK39016
33	134.6	23.2	636	5	AAH48169
34	134.6	23.2	702	5	AAH43464
35	134.6	23.2	926	2	AAQ81698
36	134.6	23.2	926	2	AAT40079
37	134.6	23.2	926	3	AAZ93614
38	134.6	23.2	926	3	AAZ93614
39	134.6	23.2	926	4	AAZ93614
40	134.6	23.2	926	6	ABK94766
41	134.6	23.2	926	7	ABT16641
42	134.6	23.2	926	9	ADD56779
43	134.6	23.2	1236	5	AAZ00247
44	134.6	23.2	7372	2	AAZ33182
45	131.8	22.7	1742	4	AAZ75960

ALIGNMENTS

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AC	AAZ96578;
XX	
DT	22-APR-1998 (first entry)
XX	
DE	Mouse bcl-w DNA.
XX	
KM	Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KM	diagnosis; degenerative disease; ss.
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OS	Mus sp.
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FT	Key
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FT	1..507
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XX	W09735971-A1.
XX	
PD	02-OCT-1997.
XX	
PE	27-MAR-1997; 97MO-AU000199.
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PR	27-MAR-1996; 96AU-00008965.
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PA	(AMRA-) AMRAD OPERATIONS PTY LTD.
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PI	Cory S Adams JM, Gibson LM, Holmgren SP;
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DR	WPI; 1997-489635/45.
XX	
PT	P-PSDB; AAW36048.
XX	
PT	Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases.
XX	
PS	Claim 3; Page 50-51; 86pp; English.
XX	
CC	This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,

Db 421 AGTGGCGCTGGCGGACCTTACAGCTTATACGGGAGCGGGCCCTGGAGGACGACCG 480
QY 481 CGTCTCGGGAGGGCAACTGGGCGATAGAGACAGTGTGTACCGGGGGCCGTGGACTG 540
Db 481 CGTCTCGGGAGGGCAACTGGGCGATAGAGACAGTGTGTACCGGGGGCCGTGGACTG 540
QY 541 GGGGCCCTGTGTAAGTGTAGAGGGGCTTTTGTGTAGCAAGTG 581
Db 541 GGGGCCCTGTGTAAGTGTAGAGGGGCTTTTGTGTAGCAAGTG 581

RESULT 3
AAK25133
ID AAK25133 standard; DNA; 581 BP.
XX
AC AAK25133;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse bcl-w gene.
XX
KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; ss.
XX
OS Mus sp.
XX
PN MO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98MO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Cory S, Adams J, Print C, Gibson L, Koentgen J;
XX
DR WPI; 1999-243890/20.
DR P-PSDB; AAY05531.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w.
XX
PS Claim 3; Page 34; 52pp; English.
XX
CC The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see
CC AAY05531), a pro-survival member of the Bcl-2 family which is widely
CC expressed and which is essential for spermatogenesis. The invention
CC relates generally to a method of treatment and to an animal model for the
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for the
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation in at least one
CC allele of the human or murine bcl-w gene or in a gene associated with bcl
CC -w. Such animals have disorganised seminiferous tubules and are
CC substantially infertile, but possess no other major abnormalities as
CC determined by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of inducing,
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
CC can induce infertility
XX
SQ Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 96.4%; Score 560.2; DB 2; Length 581;
Best Local Similarity 97.8%; Pred. No. 2.7e-142;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGCCGACCCGACCTTCAACCCCGACACACCGGCTCTAGTGGCTGACTTTGTAGCTAT 60
Db 1 ATGGGACCCCGACCTTCAACCCCGACACACCGGCTCTAGTGGCTGACTTTGTAGCTAT 60
QY 61 AGGCTGAGGCGAAGGTTATGTCTGTGAGCTGGGCGCTGGGGAAGGCCCGCCGAC 120

Db 61 AAGCTGAGGCGAAGGTTATGTCTGTGAGCTGGGCGCTGGGGAAGGCCCGCCGAC 120
QY 121 CGGCTGACCAAGCCATGCGGGCTGTGAGACAGATTGTAGACCCGTTTCCGCGAC 180
Db 121 CGGCTGACCAAGCCATGCGGGCTGTGAGACAGATTGTAGACCCGTTTCCGCGAC 180
QY 181 TTCTGTACCTGGGCGGCTGACGTACAGTACCCCGACGCTCAGCCGACAGCGTTTACC 240
Db 181 TTCTGTACCTGGGCGGCTGACGTACAGTACCCCGACGCTCAGCCGACAGCGTTTACC 240
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTTT 300
Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTTT 300
QY 301 GTCTTTGGGGCTGGCCCTGTGTGTCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGGA 360
Db 301 GTCTTTGGGGCTGGCCCTGTGTGTCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGGA 360
QY 361 CAAGTCAGAGATTGATCTGTGCTTACCTGAGACAGCTGTGCTGACTGATTCACAGC 420
Db 361 CAAGTCAGAGATTGATCTGTGCTTACCTGAGACAGCTGTGCTGACTGATTCACAGC 420
QY 421 AGTGGCGGCTGGGCGGACCTTACAGCTTATACGGGGAAGGGGCGCTGGAGGACGACCG 480
Db 421 AGTGGGCGCTGGGCGGAGTTTCAAGCTTATACGGGGAAGGGGCGCTGGAGGACGACCG 480
QY 481 CGTCTGCGGAGGCAACTGGGCGATGAGAGCAAGTGTGACGGGGGCGCTGGCACTG 540
Db 481 CGTCTGCGGAGGGAAGTGGGCGATGAGAGCAAGTGTGACGGGGGCGCTGGCACTG 540
QY 541 GGGGCCCTGTGTAAGTGTAGAGGGGCTTTTGTGTAGCAAGTG 581
Db 541 GGGGCCCTGTGTAAGTGTAGAGGGGCTTTTGTGTAGCAAGTG 581

RESULT 4
ADB52996
ID ADB52996 standard; DNA; 582 BP.
XX
AC ADB52996;
XX
DT 04-DEC-2003 (first entry)
XX
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.
XX
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
XX primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS Rattus norvegicus.
XX
PN W02003065993-A2.
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003MO-US003482.
XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378655P.
PR 09-JUL-2002; 2002US-0394230P.

PA	(GENE-)	GENE LOGIC INC.
XX		
PR	26-JAN-2003;	2003US-0442900P.
PR	04-SEP-2002;	2002US-0407688P.
PR	09-JUL-2002;	2002US-03944253P

PI Jomardrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M,
PI Elashoff M;
XX
WPI; 2003-731472/69.
DR

PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values

PS Claim 44; SEQ ID NO 3538; 874pp; English.

CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 582 BP, 111 A, 157 C, 200 G, 114 T, 0 U, 0 Other;

Query Match	93.7%;	Score 544.2;	DB 9;	Length 582;
Best Local Similarity	96.0%;	Pred. No. 6.1e-138;		
Matches 558; Conservative	0;	Mismatches 23;	Indels 0;	Gaps 0;

QY	1	ATGCCACCCCAAGCTTCAACCCCAAGACAACGCGCTCTAGTGGCTGAATTTGTAGAGCTAT	60
Db	1	ATGGCAACCCCAAGCTTCAACCCCAAGACAACGCGGCTCTAGTGGCTGAATTTGTAGAGCTAT	60
QY	61	AGGCTGAGGCAGAGGGGTTATGTCTGTGGAGCTGGGCGCTTGAGGAGGCCACGCCCGAC	120
Db	61	AAAGCTGAGGCAGAGGGGTTATGTCTGTGGAGCTGGGCGCTTGAGGAGGCCACGCCCGAC	120
QY	121	CGCGTGCACCAAGCCATGCGGGGCTGTGTGGAGCAGATTGAGACCCGTTTCCGCGCAC	180
Db	121	CCGCTGCACCAAGCCATGCGGGGAGCTGGAGCAGATTGAGACCCGTTTCCGCGCAC	180
QY	181	TTCTCTGACCTGGCGCGCTCAGCTACACGTGACGCCAGGCTCAGCCACAGACGGTTCAAC	240
Db	181	TTCTCTGACCTGGCGCGCTCAGCTACACGTGACGCCAGGCTCAGCCACAGACGGTTCAAC	240
QY	241	CAGATTTCGACCAATTTTCCAGAGGGGCGCTTAACTGGGGCGCTTGTGGCACTTTT	300
Db	241	CAGATTTCGACCAATTTTCCAGAGGGGCGCTTAACTGGGGCGCTTGTGGCACTTTT	300
QY	301	GTCTTTGGGGCTGCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGAGCTTTGTGGGA	360
Db	301	GTCTTTGGGGCTGCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGAGCTTTGTGGGA	360
QY	361	CAGATCCAGATTTGATTCGTGGGCTTACCTGGAGACAAGCTTGGCGTGAATGATCCAGC	420
Db	361	CAAGTCCAGATTTGATTTGATGACTTACCTGGAGACAAGCTTGGCGTGAATGATCCAGC	420
QY	421	AGTGGCGGCTGGGCGGACTTCAACAGCTTATTCGGGGACGGGCGCTTGGAGAGCGCACGG	480
Db	421	AGTGGGGGCTGGGCGGAGTTCAACAGCTTATTCGGGGACGGGCGCTTGGAGAGGCGACGG	480
QY	481	CGTCTGGGAGGGGCAACTGGGCAATGATGAGACAAGTGTGACGGGGGCGTGGCACTG	540

Db 481 CGTCTGGGAGAGGGGAACTGGGCACTAGTAGAGAACTGAGAGGGGGCTGTGGCACTG 540

Qy 541 GGGGCGCTGTAACTGTAGGGGCTTTTCTAGCAAGTG 581
|||||
541 GGGGCGCTGTAACTGTAGGGGCTTTTCTAGCAAGTG 581

RESULT 5	
AAV28333	
ID	AAV28333 standard; cDNA; 579 BP.

DT 02-OCT-1998 (first entry)

Rat bcl-y gene.

ss; bcl-1-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.

OS Rattus sp.

	Key	Location/Qualifiers
FH	CDS	1. .579
FT		

```
FT      /product= "bcl-y"  
FT      /note= "No stop codon given"
```

PN US5789201-A.

PD 04-AUG-1998.

PF 11-FEB-1997; 97US-00798897.

PR 23-FEB-1996; 96US-0012201P.

PA (COCE-) COCENSYS INC.

PI Guastella J,

DR WPI; 1998-446079/38.

XX
33

PT	recombinant
PT	recombinant

PS Claim 2; Column 13/14; 27pp; English.

The mammalian bcl-2 genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-2 falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired

sq sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;

Query Match	93.0%	Pred. 540.6	DB 2	Length 579
Best Local Similarity	95.9%	Pred. NO. 5.8e-137		
Matches 555	Conservative 0	Mismatches 24	Indels 0	Gaps 0

Qy 1 ATGCGAACCACAGCCCTCAACCACACAGCGCTCATGCGCTACTTTGATGGCTAT 60
Db 1 ATGCGAACCACAGCCCTCAACCACACAGCGCTCATGCGCTACTTTGATGGCTAT 60
Qy 61 AGCGCTAGGACAGAGGGTATGTCGTGGAGCTGGGCTGGGGAGAGCCAGCCCGGCAC 120
Db 61 AACCTAGACAGAGGGTATGTCGTGGAGCTGGGCTGGGGAGAGCCAGCAGCGGAC 120
Qy 121 CGCGTGCACCAAGCATGCGGCTGCTGGAGACGAGTTGAGACCCGTTTCGCGCGAC 180

Db 121 CCGCTGACACCAAGCCATGCGGGGAGAGACAGATTGAGACCCCGCTTCCGGGCGAC 180
QY 181 TTCTCTGACCTGGCCGCTCAGCTACACAGTGAACCCAGGCTCAGCCAGCAAGCTTAC 240
Db 181 TTCTCTGACCTGGCCGCTCAGCTACACAGTGAACCCAGGCTCAGCCAGCAAGCTTAC 240
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAATGAGGCGCTTTGTCATTCTT 300
Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAATGAGGCGCTTTGTCATTCTT 300
QY 301 GTCTTTGGGAGCTCCCTGTGTGCTGAGAGTCAAGAAATGAGAGCTTTGATGGA 360
Db 301 GTCTTTGGGAGCTCCCTGTGTGCTGAGAGTCAAGAAATGAGAGCTTTGATGGA 360
QY 361 CAAATCCAGGATTGATTCGTGAGCTTCACTGAGACACGCTGTGCTGACTGATCCAGC 420
Db 361 CAAATCCAGGATTGATTCGTGAGCTTCACTGAGACACGCTGTGCTGACTGATCCAGC 420
QY 421 AGTGGCGGCTGGGCGGACTTCAAGCTCTATACGGGGACGGGCGCTTGAAGACGACGG 480
Db 421 AGTGGCGGCTGGGCGGACTTCAAGCTCTATACGGGGACGGGCGCTTGAAGACGACGG 480
QY 481 CGTCTGCGGAGGAGGAGCACTGGGAGTGAAGAGACAGTGTGACCGGGCGCTTGGCAG 540
Db 481 CGTCTGCGGAGGAGGAGCACTGGGAGTGAAGAGACAGTGTGACCGGGCGCTTGGCAG 540
QY 541 GGGGCGCTGTAACTGTAGAGGCGCTTTTGTGCTAGCAG 579
Db 541 GGGGCGCTGTAACTGTAGAGGCGCTTTTGTGCTAGCAG 579

RESULT 6
AA15945
ID AA15945 standard; cDNA; 579 BP.
XX AA15945;
AC AA15945;
XX
XX
XX 20-MAY-1999 (first entry)
DE cDNA encoding the rat bcl-y protein.
XX
XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM multiple sclerosis; myocardial infarction; vitally induced cell death;
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM premature cell death; cell death stimulator; prolonged cell life span;
KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
KM ss.
XX
XX Rattus sp.
OS
XX
XX US883229-A.
PN
XX
XX 16-MAR-1999.
PD
XX
XX 25-NOV-1997; 97US-00978523.
PF
XX
XX 23-FEB-1996; 96US-0012201P.
PR
XX 11-FEB-1997; 97US-00798897.
PR
XX
XX (COCE-) COCEMSYS INC.
PA
XX
XX Guastella J;
PI
XX
XX WPI; 1999-214150/18.
DR
XX
XX P-PSDB; AAM97391.
DR
XX
XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
XX
XX Disclosure; Col 13-16; 26pp; English.
XX

CC The present sequence encodes rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
XX
Query Match 93.0%; Score 540.6; DB 2; Length 579;
Best Local Similarity 95.9%; Pred. No. 5.8e-137;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 ATGCCGACCCAGGCTCAACCCAGACACAGGCTTATGAGCTGACTTGTAGGCTAT 60
Db 1 ATGCCGACCCAGGCTCAACCCAGACACAGGCTTATGAGCTGACTTGTAGGCTAT 60
QY 61 AAGCTGAGAGCAAGAGGTTATGCTGTGAGCTGGGCGCTTGGGAGAGCCGCGGAC 120
Db 61 AAGCTGAGAGCAAGAGGTTATGCTGTGAGCTGGGCGCTTGGGAGAGCCGCGGAC 120
QY 121 CCGCTGACCAAGCCATGCGGCGCTGTGAGAGAGAGTTTGAACCCGTTCCGCGGAC 180
Db 121 CCGCTGACCAAGCCATGCGGCGCTGTGAGAGAGAGTTTGAACCCGTTCCGCGGAC 180
QY 181 TTCTCTGACCTGGGCGGCTCAGCTACACGTAACCCAGGCTCAGCCAGCAAGCTTAC 240
Db 181 TTCTCTGACCTGGGCGGCTCAGCTACACGTAACCCAGGCTCAGCCAGCAAGCTTAC 240
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAATGAGGCGCTTTGTCATTCTT 300
Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAATGAGGCGCTTTGTCATTCTT 300
QY 301 GTCTTTGGGAGCTCCCTGTGTGCTGAGAGTCAAGAAATGAGAGCTTTGATGGA 360
Db 301 GTCTTTGGGAGCTCCCTGTGTGCTGAGAGTCAAGAAATGAGAGCTTTGATGGA 360
QY 361 CAAATCCAGGATTGATTCGTGAGCTTCACTGAGACACGCTGTGCTGACTGATCCAGC 420
Db 361 CAAATCCAGGATTGATTCGTGAGCTTCACTGAGACACGCTGTGCTGACTGATCCAGC 420
QY 421 AGTGGCGGCTGGGCGGACTTCAAGCTCTATACGGGGACGGGCGCTTGAAGACGACGG 480
Db 421 AGTGGCGGCTGGGCGGACTTCAAGCTCTATACGGGGACGGGCGCTTGAAGACGACGG 480
QY 481 CGTCTGCGGAGGAGGAGCACTGGGAGTGAAGAGACAGTGTGACCGGGCGCTTGGCAG 540
Db 481 CGTCTGCGGAGGAGGAGCACTGGGAGTGAAGAGACAGTGTGACCGGGCGCTTGGCAG 540
QY 541 GGGGCGCTGTAACTGTAGAGGCGCTTTTGTGCTAGCAG 579
Db 541 GGGGCGCTGTAACTGTAGAGGCGCTTTTGTGCTAGCAG 579

RESULT 7
ABV78153
ID ABV78153 standard; DNA; 582 BP.
XX ABV78153;
AC ABV78153;
XX
XX 15-NOV-2002 (first entry)
DT

```
XX Human bcl-w DNA SEQ ID NO 37.
DE
XX RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KM
XX vitruicide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
XX W0200255693-A2.
XX
XX 18-JUL-2002.
XX
XX 09-JAN-2002; 2002WO-EP000152.
XX
XX 09-JAN-2001; 2001DE-01000586.
XX
XX 26-OCT-2001; 2001DE-01055280.
XX
XX 29-NOV-2001; 2001DE-01058411.
XX
XX 07-DEC-2001; 2001DE-01060151.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
XX
XX Inhibiting expression of target gene, useful e.g. for inhibiting
XX
XX PT oncogenes, by administering double-stranded RNA complementary to the
XX
XX PT target and having an overhang.
XX
XX
XX Claim 10; Page 134; 203pp; German.
XX
XX
XX The invention relates to inhibiting expression of a target gene (I) in a
XX
XX cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
XX
XX structure of at most 49 consecutive bases. At least part of one strand
XX
XX (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1
XX
XX has an overhang of 1-4 nucleotides. The method is used to inhibit the
XX
XX expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
XX
XX CC in humans, also genes in plasmodium or in viruses or viroids that are
XX
XX CC pathogenic for humans, animals or plants. Introducing an overhang into
XX
XX CC dsRNA greatly increases effectiveness for inhibiting gene expression.
XX
XX CC both in vivo and in vitro and also increases stability and thus the
XX
XX CC effective concentration inside the cell. The present sequence is that of
XX
XX CC a gene related to the invention
XX
XX
XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
XX
XX
XX Query Match 87.1%; Score 505.8; DB 6; Length 582;
XX
XX Best Local Similarity 91.9%; Pred. No. 1.7e-127;
XX
XX Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
XX
XX
XX 1 ATGCCGACCCCGAGCTCAACCCGACACACAGCGCTCTAGGCTGACTTTGAGGCTAT 60
XX
XX 1 ATGCCGACCCCGAGCTCTGGCCGACACACAGCGCTCTGTTGGCAGACTTTGAGGCTAT 60
XX
XX
XX 61 AGGCTGAGGACGAGGCTTATCTGTGAGCTGGGCTGAGGAGCCGACGCGCGAC 120
XX
XX 61 AAGCTGAGGACGAGGCTTATCTGTGAGCTGGCCCGGAGGCGCCACGACGCTGAC 120
XX
XX
XX 121 CCGCTGACACCAAGCCATGCGGCGCTGCTGAGACGAGTTTGAAGCCGTTCCCGCCGACC 180
XX
XX 121 CCGCTGACACCAAGCCATGCGGCGCTGAGATGATTCAGACCCGCTTCCGCGGACCC 180
XX
XX
XX 181 TTCTCTAATCTGGCGGCTCAGCTCAGCTGATGACCCCAAGCTCAGCCGACGCTTCACC 240
XX
XX 181 TTCTCTAATCTGGCGGCTCAGCTCAGCTGATGACCCCAAGCTCAGCCGACGCTTCACC 240
XX
XX
XX 241 CAGGTTCCGACGAGACTTTTTCAGAGGGGCGCTTAAGTGGGCGATTTCTTT 300
XX
XX 241 CAGGTTCCGACGAGACTTTTTCAGAGGGGCGCCCAACTGGGCGCCCTTTGAGCTTTCTTT 300
XX
XX
XX 301 GTCTTTGGGGCTGCTGTGTGTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
XX
XX 301 GTCTTTGGGGCTGACGTGTGTGTGAGAGTGTCAACAAGAGATGAGAACCACTGTGGGA 360
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XX 361 CAACTCCAGAGATTGATCGTGGCTTACCTGAGAGACAGCTGTGCTGACTGATCCAGAC 420
XX
XX 361 CAACTGCGAGAGTGTGATGTGGCTTACCTGAGAGACGCGGCTGCTGACTGATCCAGAC 420
XX
XX
XX 421 AGTGCGGCTGCGGCGGAGACTTCAAGCTTATACCGGAGACGCGGCGCTGAGAGACGACG 480
XX
XX 421 AGTGCGGCTGCGGCGGAGACTTCAAGCTTATACCGGAGACGCGGCGCTGAGAGACGCGG 480
XX
XX
XX 481 CGTCTGCGGAGAGGCACTGCGCATGAGTGAACAGCAGTGTGACGCGGCGCTGCGACTG 540
XX
XX 481 CGTCTGCGGAGAGGCACTGCGCATGAGTGAACAGCAGTGTGACGCGGCGCTGCGACTG 540
XX
XX
XX 541 GGGGCGCTGTACTGTATGAGGCGCTTTTCTGTGCAAGTG 581
XX
XX 541 GGGGCGCTGTACTGTATGAGGCGCTTTTCTGTGCAAGTG 581
XX
XX
XX RESULT 8
XX
XX ID AB235729 standard; DNA; 582 BP.
XX
XX AC AB235729;
XX
XX DT 07-FEB-2003 (first entry)
XX
XX
XX Human bcl-w polynucleotide SEQ ID NO 37.
XX
XX
XX Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; vitruicide;
XX
XX KM protozoacide; gene expression; antisense; tumour; infection; plasmodium;
XX
XX KM virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
XX
XX KM Hepatitis C virus; human papilloma virus; gene; ds.
XX
XX OS Homo sapiens.
XX
XX
XX DE10100586-A1.
XX
XX
XX 18-JUL-2002.
XX
XX
XX 09-JAN-2001; 2001DE-01000586.
XX
XX
XX 09-JAN-2001; 2001DE-01000586.
XX
XX
XX (RIBO-) RIBOPHARMA AG.
XX
XX
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX
XX WPI; 2002-683450/74.
XX
XX
XX Inhibiting expression of target genes, useful e.g. for treating tumours,
XX
XX PT by introducing into cells two double-stranded RNAs that are complementary
XX
XX PT to the target.
XX
XX
XX Claim 13; Page 30-31; 100pp; German.
XX
XX
XX The invention relates to inhibiting expression of a target gene in a cell
XX
XX CC by introducing at least two oligonucleotides (dsRNA1 and II), both
XX
XX CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
XX
XX CC pairs. At least part of one strand (S1, S2) of the ds structures in each
XX
XX CC of dsRNA1 and II are complementary to regions in the target gene. The
XX
XX CC method uses antisense inhibition of gene expression using double stranded
XX
XX CC RNA inhibition (RNAi). The method is particularly used to treat tumours
XX
XX CC or infections, especially by plasmodium or viruses/viroids (pathogenic on
XX
XX CC humans, animals or plants). The method provides more effective inhibition
XX
XX CC of expression than known methods using a single dsRNA, even at very low
XX
XX CC concentrations. When dsRNA has at least one unpaired nucleotide at the
XX
XX CC end, stability (and thus effective concentration in the cell) is improved
XX
XX CC and efficiency can be increased further by pretreating the cells with
XX
XX CC interferon. The present sequence is that of a target DNA of the invention
XX
XX
XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
XX
XX
XX Query Match 87.1%; Score 505.8; DB 6; Length 582;
```

Best Local Similarity 91.9%; Pred. No. 1.7e-127; Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```
OY 1 ATGCCGACCCCAAGCCCTCAACCCAGACACAGCGCTGATGGCTGACCTTTGTAGGCTAT 60
Db 1 ATGGGAGACCCCAAGCCCTCGAGCCCAACACACAGGCTCTGTGTGGACATTTGTAGGTTAT 60
OY 61 AGCGTGAAGGACAGAGGGTTATGTCTGTGAGAGCTGGGCGCTGGGGAAAGGCCAGCCGAC 120
Db 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGAGCTGGGCGCCCGGGAGAGGCCAGACCTAC 120
OY 121 CCGCTGACACCAAGCCATGCGGGCTGTGAGACGAGTTTGAGACCCGTTTCCGCGCAC 180
Db 121 CCGCTGACACCAAGCCATGCGGGCAGCTGGAGATGATTCAGAACCCGCTCCGCGCAC 180
OY 181 TTCTCTGACCTGGCCGCTGAGCTACAGCTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
Db 181 TTCTCTGATCTGGCGCTGAGCTGACATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
OY 241 CAGGTTTCCGACGAACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300
Db 241 CAGGTTTCCGACGAACTTTTCAAGGGGCGCCCACTGGGCGCGCTTGTAGCTTTCTT 300
OY 301 GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGCTGCAACAAAGAAATGAGCCTTTGGTGG 360
Db 301 GTCTTTGGGGCTGCACTGTGTGTGCTGAGATGTCAACAAAGAAATGAGACCTGTGGGA 360
OY 361 CAACTGACAGGATTTGATCTGTGCTGACCTGAGACAGCTGTGGCTGATGATCCACAGC 420
Db 361 CAACTGACAGGATTTGATGTGTGCTGACCTGAGACAGCGCTGTGATGATCCACAGC 420
OY 421 AGTGGGCGCTGGGCGGACCTTCAAGCTCTATAAGGGGAGCGGGCGCTGGAGACGCAAG 480
Db 421 AGTGGGCGCTGGGCGGAGTTCAAGCTCTATAAGGGGAGCGGGCGCTGGAGAGGCGCGG 480
OY 481 CGCTGCGGAGGAGGCACTGGGCAATGATGAGACAGATGATGACGGGGCGCTGGACATG 540
Db 481 CGCTGCGGAGGAGGCACTGGGCAATGATGAGAGACAGATGATGACGGGGCGCTGGACATG 540
OY 541 GGGGCGCTGTGTAAGTGTAGGGGCGCTTTTGTGTAGCAAGTG 581
Db 541 GGGGCGCTGTGTAAGTGTAGGGGCGCTTTTGTGTAGCAAGTG 581
```

RESULT 9
ABX09972
ID ABX09972 standard; DNA; 582 BP.
XX

AC ABX09972;

XX 23-JAN-2003 (first entry)

XX Human bcl-w DNA fragment SEQ ID 37.

XX Oligoribonucleotide; interferon; oncogene; cytokine; id; developmental;
XX prion; inhibition; human; ds.

XX Homo sapiens.

XX DE10100587-C1.

XX 21-NOV-2002.

XX 09-JAN-2001; 2001DE-01000587.

XX 09-JAN-2001; 2001DE-01000587.

XX (RIBO-) RIBOPHARMA AG.

XX Kreutzler R, Limmer S, Roost S, Hadwiger P;

XX WPI; 2002-742209/81.

PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT introduction of complementary double-stranded oligoribonucleotide, after
PT treating the cell with interferon.

XX Disclosure; Page 35-36; 98pp; German.

CC This invention describes a novel method for inhibiting expression of a
CC target gene by introducing into the cell that contains the target gene at
CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
CC structure of not more than 49 consecutive nucleotides (nt), where at
CC least a segment of one strand of the ds structure is complementary with
CC the target gene and the cells are treated with interferon before
CC introduction of dsRNA. The method is used to inhibit expression of
CC target genes, particularly oncogenes, cytokine genes, id (not defined)
CC protein genes; developmental or prion genes, or genes expressed in
CC pathogenic organisms (particularly plasmids) or in viruses or viroids
CC (pathogenic in humans, animals or plants). Treating the cells with
CC interferon greatly increases the extent to which dsRNA can inhibit
CC expression of the target genes, and the effect is even greater when dsRNA
CC gene fragments used to illustrate the method of the invention

XX Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 87.1%; Score 505.8; DB 6; Length 582;

Best Local Similarity 91.9%; Pred. No. 1.7e-127; Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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OY 1 ATGCCGACCCCAAGCCCTCAACCCAGACACAGCGCTGATGGCTGACCTTTGTAGGCTAT 60
Db 1 ATGGGAGACCCCAAGCCCTCGAGCCCAACACACAGGCTCTGTGTGGACATTTGTAGGTTAT 60
OY 61 AGCGTGAAGGACAGAGGGTTATGTCTGTGAGAGCTGGGCGCTGGGGAAAGGCCAGCCGAC 120
Db 61 AAGCTGAGGACAGAGGGTTATGTCTGTGAGAGCTGGGCGCCCGGGAGAGGCCAGACGCTGAC 120
OY 121 CCGGTGACCAAGCAAGCTGCGGGCTGCTGAGAGAGAACTTTGAGACCCGCTTCCGCGCAC 180
Db 121 CCGGTGACCAAGCAAGCTGCGGGCAGCTGAGAGAGATGTGAGACCCGCTTCCGCGCAC 180
OY 181 TTCTCTGACCTGGCCGCTGAGCTACAGCTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
Db 181 TTCTCTGATCTGGCGCTGAGCTGACATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
OY 241 CAGGTTTCCGACGAACTTTTCCAGAGGGGCGCTTAAGTGGGCGCTTGTGGCATTTCTT 300
Db 241 CAGGTTTCCGACGAACTTTTCAAGGGGCGCCCACTGGGCGCGCTTGTAGCTTTCTT 300
OY 301 GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGCTGCAACAAAGAAATGAGCCTTTGGTGG 360
Db 301 GTCTTTGGGGCTGCACTGTGTGTGCTGAGATGTCAACAAAGAAATGAGACCTGTGGGA 360
OY 361 CAACTGACAGGATTTGATGTGTGCTGACCTGAGACAGCTGTGGCTGATGATCCACAGC 420
Db 361 CAACTGACAGGATTTGATGTGTGCTGACCTGAGACAGCGCTGTGATGATCCACAGC 420
OY 421 AGTGGGCGCTGGGCGGACCTTCAAGCTCTATAAGGGGAGCGGGCGCTGGAGACGCAAG 480
Db 421 AGTGGGCGCTGGGCGGAGTTCAAGCTCTATAAGGGGAGCGGGCGCTGGAGAGGCGCGG 480
OY 481 CGCTGCGGAGGAGGCACTGGGCAATGATGAGACAGATGATGACGGGGCGCTGGACATG 540
Db 481 CGCTGCGGAGGAGGCACTGGGCAATGATGAGAGACAGATGATGACGGGGCGCTGGACATG 540
OY 541 GGGGCGCTGTGTAAGTGTAGGGGCGCTTTTGTGTAGCAAGTG 581
Db 541 GGGGCGCTGTGTAAGTGTAGGGGCGCTTTTGTGTAGCAAGTG 581
```

RESULT 10
ABL91694
ID ABL91694 standard; DNA; 582 BP.
XX

AC	ABE91694.
XX	
DT	28-MAY-2002 (first entry)
DE	Human polynucleotide SEQ ID NO 37.
XX	
KW	Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KM	Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KX	Cytoskeletal; vincristine; protozoacide; antibacterial; ds.
OS	Homo sapiens.
PN	DE10100586-CI.
PN	
PD	11-APR-2002.
XX	
PF	09-JAN-2001; 2001DE-01000586.
XX	
PR	09-JAN-2001; 2001DE-01000586.
XX	
PA	(RIBO-) RIBOPHARMA AG.
PI	Kreutzer R, Limmer S, Rost S, Hadwiger P;
DR	WPI; 2002-270454/32.
XX	
PT	Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT	introducing double-stranded complementary oligoRNA having unpaired
PT	terminal bases.
PS	Claim 13; Page 32; 104pp; German.
XX	
CC	The invention relates to a method for inhibiting expression of a target
CC	gene (ABE91694-ABE91797) in a cell by introducing at least one
CC	oligoribonucleotide that has a double-stranded structure consisting of at
CC	least 49 sequential nucleotide pairs, with at least part of one strand
CC	complementary with the target gene and has at least one end a single-
CC	stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC	antisense inhibition of gene expression useful e.g. for treating tumors
CC	but the oligoribonucleotides may also be directed against genes present
CC	in pathogens (e.g. Plasmodium or viruses/viroids), pathogenic on humans,
CC	animals or plants) or against cytokine, Id, developmental or prion genes.
CC	The method provides more effective inhibition of gene expression than use
CC	of known oligonucleotides, probably because the unpaired overhang
CC	increases stability and thus intracellular concentration
SQ	
	Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
	Query Match 87.1%; Score 505.8; DB 6; Length 582;
	Best Local Similarity 91.9%; Pred. No. 1.7e-127;
	Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0
OY	1 ATGCCGACCAGCTCAACCCGACACACAGCGCTATGTGGTGAAGCTTTGTAGACTAT 60
DBB	1 ATGCCGACCAGCTCAACCCGACACACAGCGCTATGTGGTGAAGCTTTGTAGACTAT 60
OY	61 AGCGTGAGCAGAAGGATTATGTCCTGTGAGCTGAGGAAAGCCCAAGCCGCAC 120
DBB	61 AGCGTGAGCAGAAGGATTATGTCCTGTGAGCTGAGGAAAGCCCAAGCCGCAC 120
OY	121 CCCTGTGACCAAGCATGCGGCGCTGTGTGAGACAGATTGAGACCCGTTTCCGCGCAC 180
DBB	121 CCCTGTGACCAAGCATGCGGCGCTGTGTGAGACAGATTGAGACCCGTTTCCGCGCAC 180
OY	121 CCCTGTGACCAAGCATGCGGCGCTGTGTGAGACAGATTGAGACCCGTTTCCGCGCAC 180
DBB	121 CCCTGTGACCAAGCATGCGGCGCTGTGTGAGACAGATTGAGACCCGTTTCCGCGCAC 180
OY	181 TTCTCTGACCTGGCGCGCTGACGTACAGTGAACCCAGAGCTACGCCACAAAGCTTACC 240
DBB	181 TTCTCTGACCTGGCGCGCTGACGTACAGTGAACCCAGAGCTACGCCACAAAGCTTACC 240
OY	241 CAGGTTTCCAGCAACCTTTTCCAAGGAGGAGCCCTTAAGTGGGCGCTTTGGACATTTCTT 300
DBB	241 CAGGTTTCCAGCAACCTTTTCCAAGGAGGAGCCCTTAAGTGGGCGCTTTGGACATTTCTT 300
OY	301 GTCTTTGGGCGCTGCTGTGTGAGAGTGTACAAGAAATGAGCCTTTGGTGGGA 360

Db	301	GTCTTTGGGGCTGCAC	TGTGTGTCTAGAGTGTCAAA	GGAAGATGGAA	CCACTGGTGGGA	360
Qy	361	CAAGTCACAGATTGGA	TGATGATGGTGGCC	CTACCTGGAGACAG	GTCTGGTGTGACTGGAT	CAAGC 420
Db	361	CAAGTCACAGAGTGA	TGATGGTGTGCTTAC	CTCGAGACGCGGCT	GTGGCTTGATCTGAT	CACGC 420
Qy	421	AGTGGCGGCTGGGCG	GACCTTCACAGCTCT	TATACGGGAGCGGG	GCCTGTGAGACGCA	CGG 480
Db	421	AGTGGGGGCTGGGCG	GAGTTTCACACCTTA	TACGGGAGCGGGCC	CTGTGAGAGGCGCG	480
Qy	481	CGTCTCGGAGAGGG	CAACTCTGATGAGCA	CAGTGCTGACCGGG	CCGTGGCACTG 540	
Db	481	CGTCTCGGAGAGGG	AAGTCTGATGAGCA	CAGTGCTGACCGGG	CCGTGGCACTG 540	
Qy	541	GGGGCCCTGGTACT	GTATAGGGCCCTTT	TTTGGTACCAAGT	581	
Db	541	GGGGCCCTGGTACT	GTATAGGGCCCTTT	TTTGGTACCAAGT	581	

RESULT 11
AAK25132
ID AAK25132 standard; DNA; 581 BP.
AAK25132;
XX
XX AC
XX AAK25132;
XX
XX 05-JUL-1999 (first entry)
XX
XX DE Human bcl-w gene.
XX
XX SM Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
XX animal model; ss.
XX
XX OS Homo sapiens.
XX
XX FN MO9913710-A1.
XX
XX PD 25-MAR-1999.
XX
XX PP 16-SEP-1998; 98MO-AU000764.
XX
XX PR 16-SEP-1997; 97AU-00009228.
XX
XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
XX DR WPI; 1999-243890/20.
XX
XX DR P-PSDB; AAY05530.
XX
XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX PT protein associated with Bcl-w.
XX
XX PS Claim 3; Page 32; 52pp; English.
XX
XX
XX The present sequence is the human bcl-w gene encoding Bcl-w protein (see
CC AA005530), a pro-survival member of the Bcl-2 family which is widely
CC expressed and which is essential for spermatogenesis. The invention
CC relates generally to a method of treatment and to an animal model for
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for the
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation is at least one
CC allele of the human or murine bcl-w gene or in a gene associated with bcl-w
CC -w. Such animals have disorganized seminiferous tubules and are
CC substantially infertile, but possess no other major abnormalities as
CC determined by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of inducing,
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
XX can induce infertility
XX
XX Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;


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AC AAT96577;
XX 22-APR-1998 (first entry)
XX DE Human bcl-w DNA.
XX KM Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX KM diagnosis; degenerative disease; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT 1..582
XX FT CDS /*tag= a
XX FT /product= "bcl-w"
XX MN MO9735971-A1.
XX PD 02-OCT-1997.
XX PF 27-MAR-1997; 97WO-AU000199.
XX PR 27-MAR-1996; 96AU-00008965.
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PI Cory S, Adams JM, Gibson LM, Holmgreen SP;
XX DR MPI: 1997-489635/45.
XX DR P-PSDB; AAM36047.
XX PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
XX PT inhibit cell survival, e.g. for treatment of cancer and degenerative
XX PT diseases.
XX PS Claim 3; Page 48; 86pp; English.
XX SS This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
XX CC family, extracted from an adult brain library. This gene promotes cell
XX CC survival, so its modulation is useful in treatment of cancer or auto-
XX CC immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,
XX CC myocardial infarct, muscular degeneration, hypoxia, ischaemia, human
XX CC immunodeficiency virus infection or in cell transplants. Up-regulation of
XX CC the gene can also be used to modify cell lines cultured in vivo, e.g. to
XX CC develop new lines, to facilitate isolation of hybridomas and to increase
XX CC survival of primary explants during genetic modification. It can be used
XX CC to produce recombinant Bcl-w for therapy, diagnosis, antibody production
XX CC or screening of potential modulators
XX SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query March 86.2%; Score 501; DB 2; Length 583;
Best Local Similarity 91.4%; Pred. No. 3.4e-126;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGCCGACCCGAGCTCAACCCAGACACAGCGCTCTAGTGTGAGCTTGTAGGCTAT 60
DB 1 ATGCCGACCCGAGCTCTGCGCCCGACACACAGCGGCTCTGTGTGAGAGCTTGTAGGTTAT 60
QY 61 AGGCTGAGGCGAAGAGGTTATGTCTGTGAGACTGCGGCTTGAGGAGAGCCAGCCGCGAC 120
DB 61 AAGCTGAGGCGAAGAGGTTATGTCTGTGAGACTGCGGCTTGAGGAGAGCCAGCGCTGAC 120
QY 121 CCGCTGACACCAAGGCAATGCGGGCTGCTGAGACAGATTTAGACCCGCTTCCGCGGACC 180
DB 121 CCGCTGACACCAAGGCAATGCGGGCTGCTGAGACATAGTTGAGACCCGCTTCCGCGGACC 180
QY 181 TTCTCTGACTGGCGGCTCAGCTACAGTACCCAGGCTCAGCCGCAAGCGTTTACG 240
DB 181 TTCTCTGACTGGCGGCTCAGCTACAGTACCCAGGCTCAGCCGCAAGCGTTTACG 240
QY 241 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAACCTGAGGCGCTTGTGTGCAATTTCTT 300

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DB 241 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAACCTGAGGCGCTTGTGTGCAATTTCTT 300
QY 301 GTCCTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAGCTTTGGTGGGA 360
DB 301 CTCCTTGGGGCTGTGACTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAGCACTGGTGGGA 360
QY 361 CAAGTCCAGGAAATGGATCGTGGGCTTACCTTGAGAGACAGTCTGCTGACTGATTCACAGC 420
DB 361 CAAGTCCAGGAAATGGATCGTGGGCTTACCTTGAGAGACAGTCTGCTGACTGATTCACAGC 420
QY 421 AGTGGCGGCTGCGCGGAGCTTCAACAGCTCTATACGAGAGCGGGGCTTGAGAGACGACGCG 480
DB 421 AGTGGCGGCTGCGCGGAGCTTCAACAGCTCTATACGAGAGCGGGGCTTGAGAGAGCGCGG 480
QY 481 CGTCTGCGGAGAGGCAATGCGGCATGAGTACGACACAGTGTGACGCGGGGCGGTGGCACTG 540
DB 481 CGTCTGCGGAGAGGCAATGCGGCATGAGTACGACAGTGTGACGCGGGGCGGTGGCACTG 540
QY 541 GGGGCGCTGTACTGTAGGGGCGCTTTTGTCTAGCAAGT 581
DB 541 GGGGCGCTGTACTGTAGGGGCGCTTTTGTCTAGCAAGT 581

RESULT 14
ID AAX25134
ID AAX25134 standard; DNA; 583 BP.
AC AAX25134;
XX 05-JUL-1999 (first entry)
XX DT 05-JUL-1999 (first entry)
XX DE Human bcl-w gene derivative.
XX KM Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
XX KM animal model; ss.
XX OS Homo sapiens.
XX SS WO9913710-A1.
XX PN WO9913710-A1.
XX PD 25-MAR-1999.
XX PF 16-SEP-1998; 98WO-AU000764.
XX PR 16-SEP-1997; 97AU-00009228.
XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX DR MPI: 1999-243890/20.
XX DR P-PSDB; AAY05532.
XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX PT protein associated with Bcl-w.
XX PS Disclosure; Page 36; 52pp; English.
XX SS The present sequence is described as a derivative of the human bcl-w gene
XX CC (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival
XX CC member of the Bcl-2 family which is widely expressed and which is
XX CC essential for spermatogenesis. The invention relates generally to a
XX CC method of treatment and to an animal model for the identification of
XX CC molecules and genetic sequences useful for inducing or reducing fertility
XX CC of male animals. Methods are provided for the treatment of infertility,
XX CC or for reducing fertility, by modulating spermatogenesis. An animal model
XX CC carries a mutation in at least one allele of the human or murine bcl-w
XX CC gene or in a gene associated with bcl-w. Such animals have disorganised
XX CC seminiferous tubules and are substantially infertile, but possess no other
XX CC major abnormalities as determined by histological examination. They can
XX CC be used to screen for therapeutic molecules including genetic sequences
XX CC capable of inducing, enhancing or otherwise facilitating spermatogenesis
XX CC in animals, or which can induce infertility

```


XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;
SQ

Query Match 86.2%; Score 501; DB 2; Length 583;
Best Local Similarity 91.4%; Pred. No. 3.4e-126;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```
QY 1 ATGCCGACCCCAAGCTTCAACCCAGACACACGCGCTGATGAGCTATGAGCTAT 60
DB 1 ATGGGAGACCCCAAGCTTCAACCCAGACACACGCGCTGATGAGCTATGAGCTAT 60
QY 61 AGCTGAGGACAGAGGGTTATGCTGTGAGAGCTGGGCGCTGGGAGGCGCCAGCCGAC 120
DB 61 AGCTGAGGACAGAGGGTTATGCTGTGAGAGCTGGGCGCTGGGAGGCGCCAGCACTGAC 120
QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTTCCGCGCAC 180
DB 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTTCCGCGCAC 180
QY 181 TTCTCTGACCTGCGCGCTCAGCTACACGTCGACCCAGCGCTCAGCCAGCAAGCTTAC 240
DB 181 TTCTCTGATCTGCGCGCTCAGCTACGTCGATGACCCAGCGCTCAGCCAGCAAGCTTAC 240
QY 241 CAGGTTTCCGACGAATTTTCCAGAGGGGCGCTTAACTGAGGCGCTTGTGTGCAATCT 300
DB 241 CAGGTTTCCGACGAATTTTCCAGAGGGGCGCTTAACTGAGGCGCGCTTGTGTGCAATCT 300
QY 301 GTCTTTGAGGCTGCGCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAGCTTTGAG 360
DB 301 GTCTTTGAGGCTGCGCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAGCTTTGAG 360
QY 361 CAAGTCCAGAGATTGATGCTGAGCTTACCTGAGAGACAGCTTGTGCTGATGATCCAGC 420
DB 361 CAAGTCCAGAGATTGATGCTGAGCTTACCTGAGAGACAGCTTGTGCTGATGATCCAGC 420
QY 421 AGTGGCGGCTGAGGAGGAGTTTCAAGCTCTATACGAGGAGCGGGCGCTTGTGAGCTT 480
DB 421 AGTGGCGGCTGAGGAGGAGTTTCAAGCTCTATACGAGGAGCGGGCGCTTGTGAGCTT 480
QY 481 CGTCTGCGGAGAGGAGCACTGAGCATGAGTGAGACAGTGTGACCGGGGCGCTGAGCACT 540
DB 481 CGTCTGCGGAGAGGAGCACTGAGCATGAGTGAGACAGTGTGACCGGGGCGCTGAGCACT 540
QY 541 GGGGCGCTGATGATGAGAGGAGCTTTTGTGCTAGCAAGTG 581
DB 541 GGGGCGCTGATGATGAGAGGAGCTTTTGTGCTAGCAAGTG 581
```

RESULT 15
AAV28334
ID AAV28334 standard; cDNA; 579 BP.

AAV28334;

02-OCT-1998 (first entry)

Human bcl-y gene.

8s; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

Homo sapiens.

Key Location/Qualifiers

FT CDS

FT 1..579
FT /tag= a
FT /product= "bcl-y"
FT /note= "No stop codon given"

US789201-A.

04-AUG-1998.

11-FEB-1997; 97US-00798897.

XX 23-FEB-1996; 96US-0012201P.
PR

PA (COCE-) COCENSYS INC.

PI Quastella J;

DR WP1; 1998-446079/38.

DR P-PSDB; AAM61392.

PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers.

PS Claim 3; Column 15/16; 27pp; English.

XX The mammalian bcl-y genes encode a protein that is a member of the bcl-2

CC family, components in the cell death pathway. The bcl-2 family have both

CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in

CC the apoptosis activity category. The recombinant protein may be used to

CC prevent uncontrolled cell growth, either by its direct administration to

CC recombinant genetic constructs to increase its expression in vivo. Also,

CC antisense constructs can be used in disorders where prevention of cell

CC death is desired

SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

Query Match 85.6%; Score 497.4; DB 2; Length 579;
Best Local Similarity 91.2%; Pred. No. 3.2e-125;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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DB 1 ATGGGAGACCCCAAGCTTCAACCCAGACACAGCGCTCTAGTGTGATCTTTGAGCTAT 60
QY 61 AGCTGAGGACAGAGGGTTATGCTGTGAGAGCTGGGCGCTGGGAGGCGCCAGCCGCGAC 120
DB 61 AGCTGAGGACAGAGGGTTATGCTGTGAGAGCTGGGCGCTGGGAGGCGCCAGCACTGAC 120
QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTTCCGCGCAC 180
DB 121 CCACTGCACCAAGCCATGCGGGCTGTGAGACGAGTTGAGACCCGTTTCCGCGCAC 180
QY 181 TTCTCTGACCTGCGCGCTCAGCTACAGCTGACCCAGCGCTCAGCCAGCAAGCTTAC 240
DB 181 TTCTCTGATCTGCGCGCTCAGCTACAGCTGACCCAGCGCTCAGCCAGCAAGCTTAC 240
QY 241 CAGGTTTCCGACGAATTTTCCAGAGGGGCGCTTAACTGAGGCGCTTGTGTGCAATCT 300
DB 241 CAGGTTTCCGACGAATTTTCCAGAGGGGCGCTTAACTGAGGCGCGCTTGTGTGCAATCT 300
QY 301 GTCTTTGAGGCTGCGCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAGCTTTGAG 360
DB 301 GTCTTTGAGGCTGCGCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGAGCTTTGAG 360
QY 361 CAAGTCCAGAGATTGATGCTGAGCTTACCTGAGAGACAGCTTGTGCTGATGATCCAGC 420
DB 361 CAAGTCCAGAGATTGATGCTGAGCTTACCTGAGAGACAGCTTGTGCTGATGATCCAGC 420
QY 421 AGTGGCGGCTGAGGAGGAGTTTCAAGCTCTATACGAGGAGCGGGCGCTTGTGAGCTT 480
DB 421 AGTGGCGGCTGAGGAGGAGTTTCAAGCTCTATACGAGGAGCGGGCGCTTGTGAGCTT 480
QY 481 CGTCTGCGGAGAGGAGCACTGAGCATGAGTGAGACAGTGTGACCGGGGCGCTGAGCACT 540
DB 481 CGTCTGCGGAGAGGAGCACTGAGCATGAGTGAGACAGTGTGACCGGGGCGCTGAGCACT 540
QY 541 GGGGCGCTGATGATGAGAGGAGCTTTTGTGCTAGCAAG 579
DB 541 GGGGCGCTGATGATGAGAGGAGCTTTTGTGCTAGCAAG 579
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Mon Mar 29 09:44:48 2004

us-09-155-327g-8.png

Page 12

Job time : 363.378 secs

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OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:20:47 ; Search time 76.3686 Seconds

(Without alignments)
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Title: US-09-155-327G-8
Perfect score: 581

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540.6	93.0	579	1 US-08-798-897-1	Sequence 1, Appli
2	540.6	93.0	579	2 US-08-798-897-1	Sequence 1, Appli
3	497.4	85.6	579	1 US-08-798-897-2	Sequence 2, Appli
4	497.4	85.6	579	2 US-08-798-897-2	Sequence 2, Appli
5	364.8	62.8	1098	4 US-09-010-147B-23	Sequence 23, Appli
6	364.4	62.7	1864	4 US-09-149-476-130	Sequence 130, App
7	134.6	23.2	926	1 US-08-081-448-5	Sequence 5, Appli
8	134.6	23.2	926	2 US-08-470-670A-6	Sequence 6, Appli
9	134.6	23.2	926	3 US-08-481-739-1	Sequence 1, Appli
10	134.6	23.2	926	3 US-09-167-921-1	Sequence 1, Appli
11	134.6	23.2	926	3 US-09-277-020-39	Sequence 39, Appli
12	134.6	23.2	926	3 US-09-323-743-1	Sequence 1, Appli
13	134.6	23.2	926	4 US-08-461-511A-5	Sequence 6, Appli
14	134.6	23.2	926	4 US-09-271-014A-5	Sequence 5, Appli
15	134.6	23.2	926	4 US-09-023-655-1430	Sequence 1430, Ap
16	134.6	23.2	926	5 PCT-US94-07089-6	Sequence 6, Appli
17	125	21.5	717	5 US-08-465-485A-20	Sequence 20, Appli
18	125	21.5	717	6 US-09-080-285-20	Sequence 20, Appli
19	125	21.5	4825	6 5459251-1	Patent No. 5459251
20	125	21.5	5086	2 US-08-465-485A-19	Sequence 19, Appli
21	125	21.5	5086	2 US-08-365-486A-14	Sequence 14, Appli
22	125	21.5	5086	3 US-09-080-285-19	Sequence 19, Appli
23	125	21.5	5086	3 US-08-880-342-14	Sequence 14, Appli
24	125	21.5	5086	4 US-09-724-426-19	Sequence 19, Appli
25	125	21.5	5086	4 US-09-233-527-7	Sequence 7, Appli
26	125	21.5	5086	4 PCT-US93-05851-4	Sequence 4, Appli
27	125	21.5	5086	5 PCT-US93-06251-2	Sequence 2, Appli

28	125	21.5	5094	4 US-09-234-186-7	Sequence 7, Appli
29	125	21.5	5104	6 5506344-1	Patent No. 5506344
30	125	21.5	6030	4 US-09-023-655-1015	Sequence 1015, Ap
31	123.4	21.2	760	4 US-08-405-702A-11	Sequence 11, Appli
32	123.4	21.2	1846	2 US-08-365-486A-16	Sequence 16, Appli
33	123.4	21.2	1846	3 US-08-880-342-16	Sequence 16, Appli
34	120.2	20.7	1274	2 US-08-470-670A-1	Sequence 1, Appli
35	120.2	20.7	1274	4 US-08-461-511A-1	Sequence 1, Appli
36	120.2	20.7	1274	5 PCT-US94-07089-1	Sequence 1, Appli
37	120.2	20.7	1303	1 US-08-081-448-1	Sequence 1, Appli
38	120.2	20.7	1303	4 US-09-271-014A-1	Sequence 1, Appli
39	119	20.5	615	2 US-08-465-485A-22	Sequence 22, Appli
40	119	20.5	615	3 US-09-080-285-22	Sequence 22, Appli
41	119	20.5	911	3 US-09-126-109-5	Sequence 5, Appli
42	119	20.5	911	5 PCT-US93-06251-3	Sequence 3, Appli
43	115.8	19.9	831	6 5459251-3	Patent No. 5459251
44	115.8	19.9	831	6 5506344-4	Patent No. 5506344
45	113.8	19.6	1384	4 US-08-899-367-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483_0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-798-897-1
;
; Query Match 93.0%; Score 540.6; DB 1; Length 579;
; Best Local Similarity 95.9%; Pred. No. 2.1e-144;
; Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
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QY 1 ATGCGAGCCAGCCTCAACCCAGACACAGCCCTAGTGTGCTGATTTGTAGCTAT 60

Db 1 ATGCGAGCCAGCCTCAACCCAGACACAGCCCTAGTGTGCTGATTTGTAGCTAT 60

QY 61 AGGCTGAGGCGAAGAGGTTATGTGTGTGAGAGCTGGGCTGGGGAAGGCCAGCCGCGAC 120

Db 61 AAGCTGAGACGAGAGGTTATGCTGTGAGAGCTGGCCCTGAGGAAAGCCAGAGCCGAC 120
Qy 121 CCGCTGACCAAGCAAGCCAGGCTGCTGAGAGCAAGTTTGAAGCCCTTTCCGCGGAC 180
Db 121 CCGCTGACCAAGCAAGCCAGGCTGAGAGCAAGTTTGAAGCCCTTTCCGCGGAC 180
Qy 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCGCAAGCTTCAC 240
Db 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCGCAAGCTTCAC 240
Qy 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGCGCTTAAGTGGGCGCTTTGTGGCAATCTTT 300
Db 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGCGCTTAAGTGGGCGCTTTGTGGCAATCTTT 300
Qy 301 GTCTTTGGGGCTGCTGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCTGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 360
Qy 361 CAAGTCCAGAGATTGATCGTGGCTACCTGGAGACAGTGTGGCTGATGATCCAGC 420
Db 361 CAAGTCCAGAGATTGATCGTGGCTACCTGGAGACAGTGTGGCTGATGATCCAGC 420
Qy 421 AGTGGCGGCTGGCGGCACTTTCACAGCTCTATACGGGAGCGGGCGCTTGGAGACGCA 480
Db 421 AGTGGCGGCTGGCGGCACTTTCACAGCTCTATACGGGAGCGGGCGCTTGGAGACGCA 480
Qy 481 CGTCTGCGGAGGAGCACTGGGCAATGATGAGACAGTGTGTGACGGGGGCGCTGGCACTG 540
Db 481 CGTCTGCGGAGGAGCACTGGGCAATGATGAGACAGTGTGTGACGGGGGCGCTGGCACTG 540
Qy 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGTAGCAAG 579
Db 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGTAGCAAG 579

RESULT 2
US-08-978-523-1
Sequence 1, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Gene Coding For Bcl-y, a Bcl-2
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-978-523-1

Query Match 93.0%; Score 540.5; DB 2; Length 579;
Best Local Similarity 95.9%; Pred. No. 2.1e-144;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ATGCCAGCCCAAGCCTCAACCCAGACACACAGCGCTCAAGTGTAGCTTGTAGGCTAT 60
Db 1 ATGCCAGCCCAAGCCTCAACCCAGACACAGCGGCTCAAGTGTAGGCTTGTAGGCTAT 60
Qy 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCTGAGGAAAGCCAGCCGAC 120
Db 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCTGAGGAAAGCCAGCCGAC 120
Qy 121 CCGCTGACCAAGCCATGCGGCGCTGCTGAGACAGAGCTTTGAGACCCGCTTCGCGGAC 180
Db 121 CCGCTGACCAAGCCATGCGGCGCTGCTGAGACAGAGCTTTGAGACCCGCTTCGCGGAC 180
Qy 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCGCAAGCTTCAC 240
Db 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCGCAAGCTTCAC 240
Qy 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGCGCTTAAGTGGGCGCTTTGTGGCAATCTTT 300
Db 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGCGCTTAAGTGGGCGCTTTGTGGCAATCTTT 300
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Db 301 GTCTTTGGGGCTGCTGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 360
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Db 361 CAAGTCCAGAGATTGATCGTGGCTACCTGGAGACAGTGTGGCTGATGATCCAGC 420
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Db 481 CGTCTGCGGAGGAGCACTGGGCAATGATGAGACAGTGTGTGACGGGGGCGCTGGCACTG 540
Qy 541 GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGTAGCAAG 579
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RESULT 3
US-08-798-897-2
Sequence 2, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Gene Coding For Bcl-y, a Bcl-2
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-798-897-2

Query Match 85.6%; Score 497.4; DB 1; Length 579;
Best Local Similarity 91.2%; Pred. No. 4e-132;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1 ATGCCGACCCAGGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGGAGCTAT 60
DB 1 ATGCCGACCCAGGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGGAGCTAT 60
QY 61 AGGCTGAGGAGAGGCTTATGCTGTGAGCTGGGCTGGGAGAGCCGACCGGAC 120
DB 61 AAGCTGAGGAGAGGCTTATGCTGTGAGCTGGGCTGGGAGAGCCGACGAGTGAC 120
QY 121 CCGCTGACCAACACCATGCGGGCTGCTGAGAGACGAGTTGAGACCCGTTCCGCGCAC 180
DB 121 CCACTGACCAACACCATGCGGGCTGCTGAGAGAGTTGAGACCCGTTCCGCGCAC 180
QY 181 TTCTCTGACCTGCGCCCTGACGCTACAGCTGACCCGAGCTCAAGCCAGAGCTTAC 240
DB 181 TTCTCTGATGCGGCTGACGCTGACGCTGACGCTGACCCGAGCTCAAGCCAGAGCTTAC 240
QY 241 CAGGTTCCGACCACTTTTCAAGGGGCGCTTAAGTGGGCGGCTTTGGACTTTT 300
DB 241 CAGGTTCCGACCACTTTTCAAGGGGCGCTTAAGTGGGCGGCTTTGGACTTTT 300
QY 301 GTCTTTGGGGCTGCTGCTGTGAGAGTGTCAACAAAGAAATGAGGCTTTGTGGGA 360
DB 301 GTCTTTGGGGCTGCTGCTGTGAGAGTGTCAACAAAGAAATGAGGCTTTGTGGGA 360
QY 361 CAACTGACAGGATGATGCTGAGCTTACCTGAGACAGCTGTGCTGACTGATCCACAC 420
DB 361 CAACTGACAGGATGATGCTGAGCTTACCTGAGACAGCTGTGCTGACTGATCCACAC 420
QY 421 AAGTGGGCGCTGGGCTGACCTTCAAGGGGCGCTTAAGTGGGCGGCTTTGGACTTT 480
DB 421 AAGTGGGCGCTGGGCTGACCTTCAAGGGGCGCTTAAGTGGGCGGCTTTGGACTTT 480
QY 481 CGTCTGCGGAGAGGAGCACTGGGCTGAGAGACAGTGTGATCGGGGCGCTTGGCACTG 540
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QY 541 GGGGCGCTGATGATCTGTAGGGGCTTTTGTGCTAGCAAG 579
DB 541 GGGGCGCTGATGATCTGTAGGGGCTTTTGTGCTAGCAAG 579

RESULT 4
US-08-978-523-2
Sequence 2, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Gustella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-978-523-2
Query Match 85.6%; Score 497.4; DB 2; Length 579;
Best Local Similarity 91.2%; Pred. No. 4e-132;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1 ATGCCGACCCAGGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGGAGCTAT 60
DB 1 ATGCCGACCCAGGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGGAGCTAT 60
QY 61 AGGCTGAGGAGAGGCTTATGCTGTGAGCTGGGCTGGGAGAGCCGACCGGAC 120
DB 61 AAGCTGAGGAGAGGCTTATGCTGTGAGCTGGGCTGGGAGAGCCGACGAGTGAC 120
QY 121 CCGCTGACCAACACCATGCGGGCTGCTGAGAGACGAGTTGAGACCCGTTCCGCGCAC 180
DB 121 CCACTGACCAACACCATGCGGGCTGCTGAGAGAGTTGAGACCCGTTCCGCGCAC 180
QY 181 TTCTCTGACCTGCGCCCTGACGCTACAGCTGACCCGAGCTCAAGCCAGAGCTTAC 240
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DB 241 CAGGTTCCGACCACTTTTCAAGGGGCGCTTAAGTGGGCGGCTTTGGACTTTT 300
QY 301 GTCTTTGGGGCTGCTGCTGTGAGAGTGTCAACAAAGAAATGAGGCTTTGTGGGA 360
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QY 361 CAACTGACAGGATGATGCTGAGCTTACCTGAGACAGCTGTGCTGACTGATCCACAC 420
DB 361 CAACTGACAGGATGATGCTGAGCTTACCTGAGACAGCTGTGCTGACTGATCCACAC 420
QY 421 AAGTGGGCGCTGGGCTGACCTTCAAGGGGCGCTTAAGTGGGCGGCTTTGGACTTT 480
DB 421 AAGTGGGCGCTGGGCTGACCTTCAAGGGGCGCTTAAGTGGGCGGCTTTGGACTTT 480

QY 481 CGTTCGCGGAGGGCACTGGGCGATGATGAGACAGTGTGTGACGGGGGCGCTGGCACTG 540
Db 481 CGTTCGCGGAGGGGAACTGGGCGATGATGAGAGACAGTGTGTGACGGGGGCGCTGGCACTG 540
QY 541 GGGGCGCGGTAACTGTAGTGGGGCGCTTTTGTCTAGCAAG 579
Db 541 GGGGCGCGGTAACTGTAGTGGGGCGCTTTTGTCTAGCAAG 579

RESULT 5

US-09-010-147B-23
Sequence 23, Application US/09010147B
Patent No. 6653445
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: Human Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.147B
FILING DATE: 12-No. 6653445-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034.205
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/034.204
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PF353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-010-147B-23

Query Match 62.8% Score 364.8; DB 4; Length 1098;
Best Local Similarity 90.3%; Pred. No. 2.6e-94;
Matches 390; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 ATGCCGACCCGAGCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 1 ATGCCGACCCGAGCTCGGCCCGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCGCTGGGAAAGGCCGCGCGAC 120
Db 61 AAGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCGCGCGGAGGCGCCGACGCTGAC 120
QY 121 CGGCTGACCAAGGCAATGCGGGCTGCTGGAGACAGATTGTAGACCCGTTTCCGCCGAC 180

Db 121 CGGCTGACCAAGGCAATGCGGGCTGCTGGAGACAGATTGTAGACCCGTTTCCGCCGAC 180
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Db 181 TTCTGTGACCTGCGGCTGACGTGATGACCCAGGCTGAGCCAGCAACGCTTCAAC 240
QY 241 CAGGTTCCGAGCAACTTTTCCAGAGGGGCGCTTAATCTGGGCGCGCTTGTGCAATTCTT 300
Db 241 CAGGTTCCGAGCAACTTTTCCAGAGGGGCGCTTAATCTGGGCGCGCTTGTGCAATTCTT 300
QY 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAATAGAGCCTTTGGTGGGA 360
Db 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAATAGAGCCTTTGGTGGGA 360
QY 361 CAAGTCCAGATTTGATGCTGGGCTTACCTGGAGACAGCTTGGCTGATGATCCAGAC 420
Db 361 CAAGTCCAGATTTGATGCTGGGCTTACCTGGAGACAGCTTGGCTGATGATCCAGAC 420
QY 421 AGTGGCGGCTGG 432
Db 421 AGTGGCGGCTGG 432

RESULT 6

US-09-149-476-130
Sequence 130, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149.476
FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040.162
FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.333
FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038.621
FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.626
FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.334
FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.336
FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.163
FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047.600
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.615
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.597
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.502
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.633
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.583
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.617
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.618
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.503
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.592
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.581
FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.584

EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 5000
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 5007
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 4927
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 5989
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 6133
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 5882
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 5968
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 6122
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 6322
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 6011
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/043, 5803
EARLIER	FILING DATE:	1997-04-11
EARLIER	APPLICATION NUMBER:	60/043, 5686
EARLIER	FILING DATE:	1997-04-11
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EARLIER	APPLICATION NUMBER:	60/043, 6599
EARLIER	FILING DATE:	1997-04-11
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EARLIER	APPLICATION NUMBER:	60/043, 3133
EARLIER	FILING DATE:	1997-04-11
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EARLIER	FILING DATE:	1997-04-11
EARLIER	APPLICATION NUMBER:	60/043, 3155
EARLIER	FILING DATE:	1997-04-11
EARLIER	APPLICATION NUMBER:	60/048, 9744
EARLIER	FILING DATE:	1997-06-06
EARLIER	APPLICATION NUMBER:	60/056, 8866
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 8777
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 8889
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 8933
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 6330
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 8788
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 6632
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 8722
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 8822
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 6377
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 9033
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 8888
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 8799
EARLIER	FILING DATE:	1997-08-22

[illegible]

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 62.7%; Score 364.4; DB 4; Length 1864;
Best Local Similarity 90.0%; Pred. No. 4,1e-94;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 1 ATGCCAGCCCAAGCTCAACCCAGACACAGCGCTAGTGTGATTTGTAGGCTAT 60
DB 11 ATGGGAGCCCAAGCTCGGCCCAAGACACAGCGCTGTGTGAGACTTTGTAGTTAT 70
QY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGTGAGCTGGGCTTGAGAGGCCAGCCGAC 120
DB 71 AAGCTGAGGCAAGAGGTTATGTCTGTGTGAGCTGGGCCGAGGAGGCGCAGCTGAC 130
QY 121 CCGCTGACCAAGCCATCGGGCTGTGAGACAGAGTTGAGACCCGTTTCCGCGGAC 180
DB 131 CCGCTGACCAAGCCATCGGGCTGTGAGACAGAGTTGAGACCCGTTTCCGCGGAC 190
QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGCTGACCCAGGCTCAGCCAGCAAGCTTACC 240
DB 191 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTACC 250
QY 241 CAGGTTTCCAGGAATTTTCCAGGGGCGCCCTAACTGGGGCGCTTTGTGGCACTCTTT 300
DB 251 CAGGCTCTCGATGAATTTTCCAGGGGCGCCCAACTGGGGCGCTTTGTGGCACTCTTT 310
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGG 360
DB 311 GTCTTTGGGGCTGTGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGAACTGGTGGGA 370
QY 361 CAGGCTCAAGGATTTGATGTGGCTCAGCTGAGAGACAGCTGTGGCTGATGTGATCCAGC 420
DB 371 CAGGCTCAAGGATTTGATGTGGCTCAGCTGAGAGACAGCTGTGGCTGATGTGATCCAGC 430
QY 421 AGTGGCGGCTGG 432
DB 431 AGTGGCGGCTGG 442

RESULT 7
US-08-081-448-5
Sequence 5, Application US/08081448
Patent No. 5646008

GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5646008th Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.

REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-081-448-5

Query Match 23.2%; Score 134.6; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGTGTGAGACAGATTGAGACCCGTTTCCGCGCACTTCTCTG 187
DB 394 AGCAAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 453
QY 188 ACCTGGCCCTCAGCTACAGCTGACCCAGGCTCAGCCAGCAAGCTTCAACCAAGTTT 247
DB 454 ACTGACATCCAGCTCCACATCACCAGGAGAGCATATCAGAGCTTTGAGACAGTAG 513
QY 248 CCGACCAATTTTCCAGGGGCGCCCTAACTGGGGCGCTTTGTGGCACTTCTTCTTTG 307
DB 514 TGAATGATCTTCCGAGATGGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 573
QY 308 GGGCTGCCCTGTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 367
DB 574 GCGGGGCACTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 633
QY 368 AGGATTTGAGGCTGTGGCTCAGCTGAGAGACAGCTGTGGCTGATGTGATCCAGCAG 427
DB 634 CAGCTTGAATGCGCACTTCACTGAATGACCACTTGAAGCTTTGATTCAGAGAAAGCG 693
QY 428 GCTGGCGGACTTCAAGCTCTTATACGGGAGCGGGCGCTGAGAGACGACGCGCTTGC 487
DB 694 GCTGGGATCTTTTGTGGAATCTTAATGGAACAATGAGACGACCGAGAGCGGAAAGG 753
QY 488 GGGAGGCAACTGGGATGATGAGACAGCTGTGTGAGCGGGCGCG 532
DB 754 AGGAACGTTCAACCGCTGTTCTGACGCGGATGATGTTGCGCG 798

RESULT 8
US-08-470-670A-6
Sequence 6, Application US/08470670A
Patent No. 5834309

GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ABCD:090--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-5000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-470-670A-6

Query Match 23.2%; Score 134.6; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 7.1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGGCTGTGAGACGAGTTTGAAGACCGTTCCGCGCACCTTCTGTG 187
DB 394 AGCAAGCGCTGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 453
QY 188 ACTGCGCCCTGACGCTACACGTCGACCCCGCTCAGCCCGAGGAGGAGGAGGAGGAGG 247
DB 454 ACCTGACATCCAGCTCCACATCACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 513
QY 248 CCGAGGACCTTTCAGAGGGGGCCCTTACTGGGGCGGCTTGTGACATTTCTTCTGTG 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGTGCATTTGTCCTTTTCTCTTCG 573
QY 308 GGGTGCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGGCTTTGGTGGGACAGTCC 367
DB 574 GCGGGGCACTGTGCGGTGAGAAAGCGTAAAGAGAGATGAGGATTTGGTGAATCGGATG 633
QY 368 AGGATGATGCTGTGCTTACTGTGAGACAGCTGTGGCTGATGATCCAGCAAGCTGGCG 427
DB 634 CAGCTTGATGCGCACTTACTGATGACCACTTGAAGCTTGTGATCCAGAGAAAGGCG 693
QY 428 GCTGGGCGGACTTTCACAGCTCTATACGGGGAGGGGGCCCTGAGAGGAGCGGCGTTCG 487
DB 694 GCTGGGATTACTTTTGTGAACTCTATGGGAACATGCAAGCCAGAGCGGAAAGGCGC 753
QY 488 GGGAGGCACTGGGAGTGAAGACAGTGTGATCCGGGGGCGG 532
DB 754 AGGAGCGCTTCAACCGCTGTTCTGAGGGGATGATGTTGGCGG 798

RESULT 9

US-08-481-739-1
Sequence 1, Application US/08481739

Patent No. 6143291
GENERAL INFORMATION:
APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,739
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,518
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RPI-034CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 135..836
US-08-481-739-1

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 7.1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGGCTGTGAGACGAGTTTGAAGACCGTTCCGCGCACCTTCTGTG 187
DB 394 AGCAAGCGCTGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 453
QY 188 ACTGCGCCCTGACGCTACACGTCGACCCCGCTCAGCCCGAGGAGGAGGAGGAGGAGG 247
DB 454 ACCTGACATCCAGCTCCACATCACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 513
QY 248 CCGAGGACCTTTCAGAGGGGGCCCTTACTGGGGCGGCTTGTGACATTTCTTCTGTG 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGTGCATTTGTCCTTTTCTCTTCG 573
QY 308 GGGTGCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGGCTTTGGTGGGACAGTCC 367
DB 574 GCGGGGCACTGTGCGGTGAGAAAGCGTAAAGAGAGATGAGGATTTGGTGAATCGGATG 633
QY 368 AGGATGATGCTGTGCTTACTGTGAGACAGTGTGGCTGATGATCCAGAGAGTGGCG 427
DB 634 CAGCTTGATGCGCACTTACTGATGACCACTTGAAGCTTGTGATCCAGAGAAAGGCG 693
QY 428 GCTGGGCGGACTTTCACAGCTCTATACGGGGAGGGGGCCCTGAGAGGAGCGGCGTTCG 487
DB 694 GCTGGGATTACTTTTGTGAACTCTATGGGAACATGCAAGCCAGAGCGGAAAGGCGC 753
QY 488 GGGAGGCACTGGGAGTGAAGACAGTGTGATCCGGGGGCGG 532
DB 754 AGGAGCGCTTCAACCGCTGTTCTGAGGGGATGATGTTGGCGG 798

RESULT 10

US-09-167-921-1
Sequence 1, Application US/09167921A

Patent No. 6172216
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Montali, Brett P.
APPLICANT: Nickoloff, Brian J.

APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 7.1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGCTGAGACGAGTTGAGACCCGTTCCGCGCACCTTCTCTG 187
DB 394 AGCAAGCGCTGAGGGAGGCGAGCGCGAGTTTGAATGCGGTACCGGCGGATTCAGTG 453
QY 188 ACCTGCGCGCTCAGCTACAGTGAACCCAGGCTCAGCCACAGCTTCACCCAGATT 247
DB 454 ACCTGACATCCAGCTCAGATCAATCACCAGGAGACAGATCAAGATCTTGAACAGGTAG 513
QY 248 CCGAAGACTTTTCCAAAGGGGCGCTTACCTGAGGCGCTTGTGGCAATCTTTGCTTTG 307
DB 514 TGAATGAACTCTTCCGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 573
QY 308 GGGCTGCGCTGTGCTGAGTGAAGTGCACAAAGAAATGAGACCTTTGGTGGACAGTCC 367
DB 574 GCGGGGCACTGTGGGTGGAAGCGTGAACAGAGATGAGATGAGATGAGTGGTGGTGG 633
QY 368 AGAATGATGATGAGGCTTACCTGAGACAGCTCTGGCTGATGATGATGATGATGATG 427
DB 634 CAGCTTGATGAGGCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATG 693
QY 428 GCTGGGCGGAGCTTCAAGCTTATACGGGGAGCGGGGCGCTGAGAGAGCGACGGCTGTG 487
DB 694 GCTGGGATATCTTTGTGGAATCTTATGGAACATATGACGACCGGAGAGCTGAAGAGG 753
QY 488 GGGAGGGCACTGGGCGATGAGTGAACAGTGTGAGCGGGGCGG 532
DB 754 AGGAAGCTTCAACCGCTGTCTTCTGAGCGGAGATGATGATGATGATGATGATGATG 798

RESULT 11
US-09-277-020-39
Sequence 39, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
US-09-277-020-39

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 7.1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGCTGAGACGAGTTGAGACCCGTTCCGCGCACCTTCTCTG 187
DB 394 AGCAAGCGCTGAGGGAGGCGAGCGCGAGTTTGAATGCGGTACCGGCGGATTCAGTG 453
QY 188 ACCTGCGCGCTCAGCTACAGTGAACCCAGGCTCAGCCACAGCTTCACCCAGATT 247
DB 454 ACCTGACATCCAGCTCAGATCAATCACCAGGAGACAGATCAAGATCTTGAACAGGTAG 513
QY 248 CCGAAGACTTTTCCAAAGGGGCGCTTACCTGAGGCGCTTGTGGCAATCTTTGCTTTG 307
DB 514 TGAATGAACTCTTCCGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 573
QY 308 GGGCTGCGCTGTGCTGAGTGAAGTGCACAAAGAAATGAGACCTTTGGTGGGACAAATCC 367
DB 574 GCGGGGCACTGTGCTGGAAGCGTGAACAGAGATGAGATGATGATGATGATGATGATG 633
QY 368 AGAATGATGATGAGGCTTACCTGAGACAGCTGTGCTGATGATGATGATGATGATGATG 427
DB 634 CAGCTTGATGAGGCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATG 693
QY 428 GCTGGGCGGACTTCAAGCTTATACGGGGAGCGGGGCGCTTGAAGAGCGACGGCTGTG 487
DB 694 GCTGGGATATCTTTGTGGAATCTTATGGGAACATATGACAGCGGAGCGGAGAGGCGC 753
QY 488 GGGAGGGCACTGGGCGATGAGTGAACAGTGTGATGAGCGGGGCGG 532
DB 754 AGGAAGCTTCAACCGCTGTCTTCTGAGCGGAGATGATGATGATGATGATGATGATG 798

RESULT 12
US-09-323-743-1
Sequence 1, Application US/09323743
Patent No. 6214986
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 7.1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGCTGAGACGAGTTGAGACCCGTTCCGCGCACCTTCTCTG 187
DB 394 AGCAAGCGCTGAGGGAGGCGAGCGCGAGTTTGAATGCGGTACCGGCGGATTCAGTG 453

QY 188 ACCGCGCCGCTACGCTACAGTGACCCGAGCTCAGCCGAGCAAGCTTACCCAGTTT 247
DB 454 ACCGCGCCGCTACGCTACAGTGACCCGAGCTCAGCCGAGCAAGCTTACCCAGTTT 513
QY 248 CCGAGCACTTTTCCAAAGGGGGCCCTTAATGCGGGCCGCTTGTGATCTTTTCTTGG 307
DB 514 TGAATGAACCTCTTCCGGGATGGGGTAACTGCGGGTGCATTTGTGCTTTTCTCTTGG 573
QY 308 GGGCTGCCCTGTGTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGCGGACAAGTCC 367
DB 574 GCGGGGCACTGTGCTGTGGAAGAGTGAAGAGAGATGAGGATTTGTGATCGGATCG 633
QY 368 AGGATTGATCGTGGCTTAAGCTGAGACACGCTGCTGATCTGATTCACAGCAAGTGGCG 427
DB 634 CAGCTTGATGAGCACTTAAGCTGAGAGACCACTTAAGCTTGTGATTCAGAGAGAGCGGCG 693
QY 428 GCTGGGCGGACTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGAGCGCTTGC 487
DB 694 GCTGGGATACCTTTTGTGAACTCTATGAGCAATGACAGCAGCCGAGAGCGGAGCGCC 753
QY 488 GGGAGGGCAACTGGGATGAGTGAACAGTGTGACGGGGGCGG 532
DB 754 AGGAGCGCTTCAACCGCTGCTTCTGACGGGCAATGATGTGGCG 798

RESULT 13
US-08-461-511A-6
Sequence 6, Application US/08461511A
Patent No. 6303331

GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.B.
Boise, Lawrence H.

TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
AND METHODS

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A

FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN

ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 135..836

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-461-511A-6

Query Match 23.2%; Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAGGCAATGCGGGCTGTGAGAGAGATTGAGACCCGTTTCCGCGGACCTTCTTG 187
DB 394 AGGAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
QY 188 ACCGCGCCGCTACGCTACAGTGAACCCAGGCTCAGCCAGCAAGCTTACCCAGTTT 247
DB 454 ACCGCGCCGCTACGCTACAGTGAACCCAGGCTCAGCCAGGAGGAGGAGGAGGAGGAGGAG 513
QY 248 CCGAGCACTTTTCCAAAGGGGGCCCTTAATGCGGGCCGCTTGTGATCTTTTCTTGG 307
DB 514 TGAATGAACCTCTTCCGGGATGGGGTAACTGCGGGTGCATTTGTGCTTTTCTCTTGG 573
QY 308 GGGCTGCCCTGTGTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGCGGACAAGTCC 367
DB 574 GCGGGGCACTGTGCTGTGGAAGAGTGAAGAGAGATGAGGATTTGTGATCGGATCG 633
QY 368 AGGATTGATCGTGGCTTAAGCTGAGACACGCTGCTGATCTGATTCACAGCAAGTGGCG 427
DB 634 CAGCTTGATGAGCACTTAAGCTGAGAGACCACTTAAGCTTGTGATTCAGAGAGAGCGGCG 693
QY 428 GCTGGGCGGACTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGAGCGCTTGC 487
DB 694 GCTGGGATACCTTTTGTGAACTCTATGAGCAATGACAGAGCGGAGCGCGGAGCGCC 753
QY 488 GGGAGGGCAACTGGGATGAGTGAACAGTGTGACGGGGGCGG 532
DB 754 AGGAGCGCTTCAACCGCTGCTTCTGACGGGCAATGATGTGGCG 798

RESULT 14
US-09-271-014A-5
Sequence 5, Application US/09271014A
Patent No. 6395510

GENERAL INFORMATION:
APPLICANT: THOMPSON, CRAIG B.
Boise, Lawrence H.

TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:316

CURRENT APPLICATION NUMBER: US/09/271,014A
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent Ver. 2.1

SEQ ID NO 5
LENGTH: 926

TYPE: DNA
ORGANISM: Human

FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)

US-09-271-014A-5

Query Match 23.2%; Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAGGCAATGCGGGCTGTGAGAGAGATTGAGACCCGTTTCCGCGGACCTTCTTG 187
DB 394 AGGAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
QY 188 ACCGCGCCGCTACGCTACAGTGAACCCAGGCTCAGCCAGCAAGCTTACCCAGTTT 247
DB 454 ACCGCGCCGCTACGCTACAGTGAACCCAGGCTCAGCCAGGAGGAGGAGGAGGAGGAGGAG 513
QY 248 CCGAGCACTTTTCCAAAGGGGGCCCTTAATGCGGGCCGCTTGTGATCTTTTCTTGG 307
DB 514 TGAATGAACCTCTTCCGGGATGGGGTAACTGCGGGTGCATTTGTGCTTTTCTCTTGG 573
QY 308 GGGCTGCCCTGTGTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGCGGACAAGTCC 367
DB 574 GCGGGGCACTGTGCTGTGGAAGAGTGAAGAGAGATGAGGATTTGTGATCGGATCG 633
QY 368 AGGATTGATCGTGGCTTAAGCTGAGACACGCTGCTGATCTGATTCACAGCAAGTGGCG 427

Db 634 CAGTTGATGGCACTTACCTGATGACCACTAGAGCTTGTGATCCAGAGACGGCG 693
QY 428 GCTGGGCGGACTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGCAAGCCCTCTCG 487
Db 694 GCTGGGATCTTTTGTGGAATCTATGGGAACATGACAGCGCCGAGAGCCGAAAGGCC 753
QY 488 GGGAGGCGCACTGGGATGAGTGAAGCAAGTGGTGAACGGGGGCCG 532
Db 754 AGGAACCTTCAACCGCTGTTCTGTACGGGCACTGACTGTGGCCG 798

RESULT 15

US-09-023-655-1430
Sequence 1430, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0595
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1430:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g510900
US-09-023-655-1430

Query Match

23.2%; Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGGAGACGATTTGAGACCCGTTTCCGCCGCACTTCTCTG 187
Db 394 AGCAAGCGCTGAGGAGGAGGAGCGAGGATTTGAATGCGGATCCGGCGGCAATTCAGTG 453
QY 188 ACCTGGCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGCAAGCTTCAACCAGGTTT 247
Db 454 ACCTGACATCCACGCTCCACATCAACCCAGGAGACAGCATATCAGAGCTTTGAAACAGTAG 513

QY 248 CCGAGCACTTTCCAAAGGGGCCCCCTAAGTGGGGCCGCTTGTGGCATCTTGTCTTTG 307
Db 514 TGAATGAACCTTCCGGGATGGGGTAACTGGGGTCCATTTGGCTTTTCTTCCTTG 573
QY 308 GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGACAACTCC 367
Db 574 GCGGGGCACTGTGTGGGAAAGCGTAGAACAGGATGACAGTATGATGATGAGATCG 633
QY 368 AGAATTGATGATGCGCTACCTGAGACAGCTGTGCTGATCGATCCACAGCAGTGGCG 427
Db 634 CAGCTTGAATGCCACTTACTGATGACCACTAGAGCCTTGGATCCAGAGAACGGCG 693
QY 428 GCTGGGCGGACTTCACAGCTCTATACGGGAGCGGGCCCTGAGAGACGACGCGGTCTGC 487
Db 694 GCTGGGATCTTTTGTGGAATCTATGGGAACATGACAGCGCCGAGAGCCGAAAGGCC 753
QY 488 GGGAGGCGCACTGGGCACTGAGTGAAGCAAGTGGTGAACGGGGGCCG 532
Db 754 AGGAACGCTTCAACCGCTGTTCTGTACGGGCACTGACTGTGGCCG 798

Search completed: March 29, 2004, 07:30:35
Job time : 78.3686 secs

GenCore version 5.1.6
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OM protein-- protein search, using sw model

Run on: March 25, 2004, 15:35:20 ; Search time 36 Seconds

(without alignments)
1691.528 Million cell updates/sec

Title: US-09-155-327g-9

Perfect score: 1009
Sequence: 1 MATPASTPDRALVADPVGY.....LTGAVALGALTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005	99.6	193	11	Q88996
2	1005	99.6	193	11	Q7TS60
3	965	95.6	193	11	Q8CGJ4
4	770	76.3	178	11	Q8CYW5
5	770	76.3	178	11	Q8CFR2
6	439.5	43.6	233	6	Q9MYW4
7	435.5	43.2	233	11	Q35844
8	433.5	42.9	233	6	Q8EQ42
9	431.5	42.8	233	6	Q8H1A2
10	428.5	42.5	233	6	Q9WZ57
11	412	40.8	236	11	Q8BQR4
12	412	40.8	236	11	Q7TSN8
13	405	40.2	79	11	Q7TS61
14	401	39.7	180	6	Q8BD55
15	401	39.7	217	11	Q9JN55
16	400	39.6	238	13	Q90Z98

17	398.5	39.5	180	6	Q9BDX7	Q9BDX7 bos taurus
18	398	39.4	236	11	Q9Z3R6	Q9Z3R6 cricetus
19	395.5	39.2	235	6	Q81008	Q81008 felis silve
20	380.5	37.7	284	11	Q7TS62	Q7TS62 rattus norv
21	374.5	37.1	188	11	Q9QWJ2	Q9QWJ2 mus musculu
22	374.5	37.1	235	11	Q35843	Q35843 mus musculu
23	372.5	36.9	188	4	Q9H1K6	Q9H1K6 homo sapien
24	371	36.8	204	13	Q9QZM2	Q9QZM2 xenopus lae
25	365.5	36.2	153	6	Q7YRB6	Q7YRB6 canis fami
26	353	35.0	185	6	Q8WJ81	Q8WJ81 bos taurus
27	347	34.4	219	11	Q9N335	Q9N335 mus musculu
28	342.5	33.9	159	11	Q8C5P0	Q8C5P0 mus musculu
29	296	29.3	89	13	Q8WJ01	Q8WJ01 gallus gall
30	187	18.5	209	11	Q9JX59	Q9JX59 rattus norv
31	185	18.3	170	11	Q9WJ15	Q9WJ15 rattus norv
32	182	18.0	209	11	Q8C264	Q8C264 mus musculu
33	174.5	17.3	182	13	Q919N4	Q919N4 brachydario
34	172.5	17.1	221	13	Q98U13	Q98U13 xenopus lae
35	170.5	16.9	150	4	Q8NFF3	Q8NFF3 homo sapien
36	168.5	16.7	125	4	Q9H1R5	Q9H1R5 homo sapien
37	163	16.2	235	5	Q967D2	Q967D2 geodia cydo
38	162	16.1	58	11	Q9R1B3	Q9R1B3 rattus norv
39	157.5	15.6	153	6	Q9WZ56	Q9WZ56 ovis aries
40	156.5	15.5	173	11	Q8K3J2	Q8K3J2 mus musculu
41	154	15.3	173	11	Q8W249	Q8W249 homo sapien
42	154	15.3	173	11	Q9JXL3	Q9JXL3 rattus norv
43	151	15.0	67	6	Q8MTB3	Q8MTB3 cervus elap
44	149	14.8	192	6	Q8SQ43	Q8SQ43 felis silve
45	148.5	14.7	218	5	Q9N754	Q9N754 suberites d

ALIGNMENTS

RESULT 1

Q88996 PRELIMINARY; PRT; 193 AA.
AC Q88996; 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Bcl-2.
GN BCL-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=9292146; PubMed=1036024;
RA Hammer S., Skoglosa Y., Lindholm D.;
RT "Differential expression of bcl-2 and bcl-x messenger RNA in the
RT developing and adult rat nervous system."; Neurosci 91:673-684 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation."; J. Neurochem. 85:1500-1512(2003).
RL J. Neurochem. 85:1500-1512(2003).
DR EMBL: AF096291; AAC64200.1; -;
DR HSBP; AY185098; AAC64468.1; -;
DR HSBP; Q07817; IMAZ.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl2; 1.
DR Pfam: PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PSS01080; BH1; 1.
DR PROSITE; PSS01258; BH2; 1.
DR PROSITE; PSS01260; BH4_1; 1.
DR PROSITE; PSS0063; BH4_2; 1.
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 99.6%; Score 1005; DB 11; Length 193;
Best Local Similarity 99.5%; Pred. No. 3.9e-81;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
QY 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
DB 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
QY 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

RESULT 2

QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
QY 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
DB 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
QY 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

Query Match 99.6%; Score 1005; DB 11; Length 219;
Best Local Similarity 99.5%; Pred. No. 4.6e-81;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 27 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 86
QY 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
DB 87 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 146
QY 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
DB 147 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 206
QY 181 GALVTVGAFPAK 193
DB 207 GALVTVGAFPAK 219

RESULT 3
QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
QY 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
DB 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
QY 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
QY 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
DB 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
QY 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

Query Match 95.6%; Score 965; DB 11; Length 193;
Best Local Similarity 96.4%; Pred. No. 1.4e-77;
Matches 186; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
QY 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
DB 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
QY 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

RESULT 4

QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
QY 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
DB 61 FSDLAAGLHVTTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLG 120
QY 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLDWIMHSSGGMAEFTLYGDDGALBEARRLRGNWASVRTLGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

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RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Adakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Asaburner M., Batalov S., Cavaant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiba H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Wasth T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlschki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RL EMBL; AK013244; BAB28740.1; -.
DR HSSP; Q07817; 1MA2.
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match 76.3%; Score 770; DB 11; Length 178;
Best Local Similarity 96.7%; Pred. No. 2,3e-60;
Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATPASTPTDRLVADFGVGYKLRQKGYVCGAGPGEPPADPLHQARRAGDEFETFRFRT 60
DB 1 MATPASTPTDRLVADFGVGYKLRQKGYVCGAGPGEPPADPLHQARRAGDEFETFRFRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDLPFGGPNWGRVLAFFVFGALCAESVKNKEPPLVG 120
DB 61 FSDLAQLHTVTPGSAQQRFTQVSDLPFGGPNWGRVLAFFVFGALCAESVKNKEPPLVG 120
QY 121 QVQDMWVAYLETRLADWIMHSSGGWAEFTAL 150
DB 121 QVQDMWVAYLETRLADWIMHSSGGWAEFTAL 150
DB 121 QVQDMWVAYLETRLADWIMHSSGGWAEFTAL 150

RESULT 5
Q8CFR2 PRELIMINARY; PRT; 178 AA.
AC Q8CFR2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB Bcl2-like 2.
GN BCL2L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;

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RL Submitted (NCV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040369; AA040369.1; -.
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;

Query Match 76.3%; Score 770; DB 11; Length 178;
Best Local Similarity 96.7%; Pred. No. 2,3e-60;
Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATPASTPTDRLVADFGVGYKLRQKGYVCGAGPGEPPADPLHQARRAGDEFETFRFRT 60
DB 1 MATPASTPTDRLVADFGVGYKLRQKGYVCGAGPGEPPADPLHQARRAGDEFETFRFRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDLPFGGPNWGRVLAFFVFGALCAESVKNKEPPLVG 120
DB 61 FSDLAQLHTVTPGSAQQRFTQVSDLPFGGPNWGRVLAFFVFGALCAESVKNKEPPLVG 120
QY 121 QVQDMWVAYLETRLADWIMHSSGGWAEFTAL 150
DB 121 QVQDMWVAYLETRLADWIMHSSGGWAEFTAL 150

RESULT 6
Q9MYT4 PRELIMINARY; PRT; 233 AA.
AC Q9MYT4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Bcl-X.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC Knecht J.C., Robertson L., James E.R.;
RA "Rabbit Bcl-X."
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY005131; AAR8137.1; -.
DR HSSP; P53563; IAF3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

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Query Match 43.6%; Score 439.5; DB 6; Length 233;
 Best Local Similarity 42.0%; Pred. No. 5,9e-31;
 Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADFGVYKLRQKGYC-----GAG-----GEGPAA 39
 DB 6 RELVDFLSYKLSQKGYMSQPSDVENRTEAPEGTGEMETPSAINGNPAMHPADSPAV 65

QY 40 D-----PLHQAMRAAGDEFTRFRFTFSDLAQLHVTGSAQQRFTQ 81
 DB 66 NGATCHSSLDAREVIPTMAVKQALREAGDEFELRYRAFSDLTSQLHITGTAYQSEBQ 125

QY 82 VSDELFGQGPWNGRLVAFVFGAALCAESVKNKEPVLGVQVQDMVAVLETRLADWTHSS 141
 DB 126 VVNELEFRDGVNMGRIVAFVFGAALCAESVDKEMEVLSRIAAMATYLNHLEPWIOEN 185

QY 142 GGMAEFTALYDGALEEARLRLE--GNVASVRYTLTGAVALGAL 183
 DB 186 GGMDFTFVLYGNNAAESKKGERNRWFLLTGMTVAGVLLGSL 229

RESULT 7
 035844 PRELIMINARY; PRT; 233 AA.

ID 035844; PRELIMINARY; PRT; 233 AA.
 AC 035844; PRELIMINARY; PRT; 233 AA.
 DT 01-JUN-1998 (TrEMBLrel. 05, Created)
 DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bcl-XL.
 GN BCL2L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/CBA; TISSUE=Thymus;
 RX MEDLINE=98051053; PubMed=9390687;
 RA Yang X.-F., Weber G.F., Cantor H.;
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates
 apoptosis in T cells";
 RL Immunity 7:629-638(1997).
 DR EMBL; U51278; AAC33459.1; -
 DR HSP; P53563; IAF3.
 DR MGD; MG1:88139; Bcl2L.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016329; P:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH4.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2-reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PSS0062; BCL2_FAMILY; 1.
 DR PROSITE; PSS01080; BH1; 1.
 DR PROSITE; PSS01258; BH2; 1.
 DR PROSITE; PSS01259; BH3; 1.
 DR PROSITE; PSS01260; BH4; 1; 1.
 DR PROSITE; PSS0063; BH4_2; 1.
 DR PROSITE; PSS0063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;

Query Match 43.2%; Score 435.5; DB 11; Length 233;
 Best Local Similarity 41.8%; Pred. No. 1.3e-30;
 Matches 94; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 11 RALVADFGVYKLRQKGY-----V 28
 DB 6 RELVDFLSYKLSQKGYMSQPSDVENRTEAPEGTGEMETPSAINGNPAMHPADSPAV 65

QY 29 CGAGPGEPPAD-----PLHQAMRAAGDEFTRFRFTFSDLAQLHVTGSAQQRFT 80
 DB 66 NGA-TGHSSSLDAREVIMPAVKQALREAGDEFELRYRAFSDLTSQLHITGTAYQSEB 124

QY 81 QVSELEFGQGPWNGRLVAFVFGAALCAESVKNKEPVLGVQVQDMVAVLETRLADWTHS 140
 DB 125 QVNELEFRDGVNMGRIVAFVFGAALCAESVDKEMEVLSRIAAMATYLNHLEPWIOE 184

QY 141 SGMMAEFTALYDGALEEARLRLE--GNVASVRYTLTGAVALGAL 183
 DB 185 NGMDTFVLYGNNAAESKKGERNRWFLLTGMTVAGVLLGSL 229

RESULT 8
 088042 PRELIMINARY; PRT; 233 AA.

ID 088042; PRELIMINARY; PRT; 233 AA.
 AC 088042; PRELIMINARY; PRT; 233 AA.
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bcl-XL protein.
 GN BCL-XL.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
 RT "Molecular cloning of feline Bcl-2 family.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB080951; BAB85856.2; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016329; P:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH4.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; BCL2_FAMILY.
 DR InterPro; IPR004725; Bcl2-reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PSS0062; BCL2_FAMILY; 1.
 DR PROSITE; PSS01080; BH1; 1.
 DR PROSITE; PSS01258; BH2; 1.
 DR PROSITE; PSS01259; BH3; 1.
 DR PROSITE; PSS01260; BH4; 1; 1.
 DR PROSITE; PSS0063; BH4_2; 1.
 DR PROSITE; PSS0063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26017 MW; CD17F24FE9D47BC9 CRC64;

Query Match 42.9%; Score 432.5; DB 6; Length 233;
 Best Local Similarity 41.6%; Pred. No. 2.5e-30;
 Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;

QY 11 RALVADFGVYKLRQKGY-----V 28
 DB 6 RELVDFLSYKLSQKGYMSQPSDVENRTEAPEGTGEMETPSAINGNPAMHPADSPAV 65

QY 29 CGAGPGEPPAD-----PLHQAMRAAGDEFTRFRFTFSDLAQLHVTGSAQQRFT 80
 DB 66 NGA-TGHSSSLDAREVIMPAVKQALREAGDEFELRYRAFSDLTSQLHITGTAYQSEB 124

QY 81 QVSELEFGQGPWNGRLVAFVFGAALCAESVKNKEPVLGVQVQDMVAVLETRLADWTHS 140
 DB 125 QVNELEFRDGVNMGRIVAFVFGAALCAESVDKEMEVLSRIAAMATYLNHLEPWIOE 184

QY 141 SGMMAEFTALYDGALEEARLRLE--GNVASVRYTLTGAVALGALGAFPAK 193
 DB 185 NGMDTFVLYGNNAAESKKGERNRWFLLTGMTVAG-VLLGLFSRK 223

RESULT 9

OSN1A2

ID Q9N1A2

PRELIMINARY;

PRT; 233 AA.

AC Q9N1A2;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Anti-apoptotic regulator Bcl-XL.

GN BCL-XL.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_Taxid=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RA Lee T.L., Cauty J.M.,

RT "PCR Cloning of a Porcine bcl-XL cDNA from Heart."

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF216205; AAF33212.1; -.

DR HSSP: Q07817; IMAZ.

DR GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0016329; F:apoptosis regulator activity; IEA.

DR GO: GO:0006915; P:apoptosis; IEA.

DR InterPro: IPR000712; Bcl2_BH.

DR InterPro: IPR003093; Bcl2_BH4.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR004725; Bcl2_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRfam: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4; 1; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_Taxid=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;

RT "Bcl-X in the sheep ovary."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF164517; AAF89532.1; -.

DR HSSP: P53563; IAF3.

DR GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0016329; F:apoptosis regulator activity; IEA.

DR GO: GO:0006915; P:apoptosis; IEA.

DR InterPro: IPR000712; Bcl2_BH.

DR InterPro: IPR003093; Bcl2_BH4.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR004725; Bcl2_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRfam: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4; 1; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR PROSITE: PS50063; BH4_2; 1.

Query Match 42.5%; Score 428.5; DB 6; Length 233;

Best Local Similarity 40.6%; Pred. No. 5; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

RL Nature 420:563-573(2002).
 DR EMBL: AK049473; BAC33767.1; -
 DR MGD: MGI:88138; Bcl2.
 DR GO: GO:0005829; Cytosol; IDA.
 DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0005915; F:apoptosis; IDA.
 DR InterPro: IPR00712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRFAMs: TIGR00865; bcl-2; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 SQ SEQUENCE 236 AA; 26437 MW; B726BFA3A1C718 CRC64;

Query Match 40.8%; Score 412; DB 11; Length 236;
 Best Local Similarity 37.5%; Pred. No. 1.6e-28;
 Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRALVADPVGKLRQKGVCGAG-----PG----- 34
 DB 10 DNRRLVATGTPALSPVPVVLTLRRAGDDPSRRYRDFAMSSQLHTPTAGRPAT 69
 QY 35 -----EGPADP-----LHQANRAAGDEFETFRPTFSDLAQLHTPTGSAQQRPTQ 81
 DB 70 SPLRLVATGTPALSPVPVVLTLRRAGDDPSRRYRDFAMSSQLHTPTAGRPAT 129
 QY 82 VSDLEFGGPNMGRVAFVFGAALCAESVNEKEPVLGVQVQDMVAVLETRLADWIISS 141
 DB 130 VVEELFRDGVNMGRIYAFEFEGVNCVSVNEMSPVNDIALMWTETYLNRHLHTWIDN 189
 QY 142 GGMAEFTALYDGALEEARLRREGNWSVRYTLTGAVLALGVYGAFFPASK 193
 DB 190 GGMDAFVELYG----PSMRPLDFSWLSIKTLISAL-VGACITUGAVLGSK 236

RESULT 12
 Q7TSN8 PRELIMINARY; PRT; 236 AA.
 AC Q7TSN8;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Bcl2-like protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RA Tanaka T.; Nangaku M.;
 RT "Rat Bcl2-like protein."
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF512835; AAK47159.1; -
 SQ SEQUENCE 236 AA; 26407 MW; 80PDCFE78C735092 CRC64;

Query Match 40.8%; Score 412; DB 11; Length 236;
 Best Local Similarity 37.5%; Pred. No. 1.6e-28;
 Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;
 QY 9 DTRALVADPVGKLRQKGVCGAG-----PG----- 34
 DB 10 DNRRLVATGTPALSPVPVVLTLRRAGDDPSRRYRDFAMSSQLHTPTAGRPAT 69

QY 35 -----EGPADP-----LHQANRAAGDEFETFRPTFSDLAQLHTPTGSAQQRPTQ 81
 DB 70 SPLRLVATGTPALSPVPVVLTLRRAGDDPSRRYRDFAMSSQLHTPTAGRPAT 129
 QY 82 VSDLEFGGPNMGRVAFVFGAALCAESVNEKEPVLGVQVQDMVAVLETRLADWIISS 141
 DB 130 VVEELFRDGVNMGRIYAFEFEGVNCVSVNEMSPVNDIALMWTETYLNRHLHTWIDN 189
 QY 142 GGMAEFTALYDGALEEARLRREGNWSVRYTLTGAVLALGVYGAFFPASK 193
 DB 190 GGMDAFVELYG----PSMRPLDFSWLSIKTLISAL-VGACITUGAVLGSK 236

RESULT 13
 Q7TS61 PRELIMINARY; PRT; 79 AA.
 ID Q7TS61;
 AC Q7TS61;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE BCL-Ws.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22672518; PubMed=12787069;
 RA Itoh T.; Itoh A.; Pleasure D.;
 RT "Bcl-2-related protein family gene expression during oligodendroglial
 RT differentiation."
 RL J. Neurochem. 85:1500-1512(2003).
 DR EMBL: AY185099; AAO64469.1; -
 SQ SEQUENCE 79 AA; 8602 MW; 47EDFB3BE2909485 CRC64;

Query Match 40.2%; Score 406; DB 11; Length 79;
 Best Local Similarity 98.7%; Pred. No. 1.4e-28;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 115 MEPLVGQVQDMVAVLETRLADWIISSGGMAEFTALYDGALEEARLRREGNWSVRYTL 174
 DB 1 MEPLVGQVQDMVAVLETRLADWIISSGGMAEFTALYDGALEEARLRREGNWSVRYTL 60
 QY 175 TGAVALGALVYGAFFPASK 193
 DB 61 TGAVALGALVYGAFFPASK 79

RESULT 14
 Q9BDS5 PRELIMINARY; PRT; 180 AA.
 ID Q9BDS5;
 AC Q9BDS5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Anti-apoptotic regulator Bcl-xL (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Amills W.; Bouzat U.;
 RT "Characterization of the bovine bcl-xL gene and related pseudogenes."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF245488; AAK31307.1; -
 DR EMBL: AF245489; AAK31308.1; -
 DR HSP; Q07817; IMAZ.
 DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO: GO:0005915; P:apoptosis; IEA.

DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR002475; BCL2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 FT NON_TER 1
 FT NON_TER 180
 SQ SEQUENCE 180 AA; 20062 MW; 95DC436F95DABDA6 CRC64;

Query Match 39.7%; Score 401; DB 6; Length 180;
 Best Local Similarity 53.5%; Pred. No. 1.1e-27;
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEFEFRFRFTSDLAQLHVTGSAQORFTQVSDELFOGQPNMGRIVAFFVFG 103
 DB 38 QALREAGDEFEFLRYRRAFSDLTSGQLHTPGTAYQSFEOYVNELFRDGVNMGRIVAFSFG 97
 QY 104 AALCAESVKNKEMEPVGVQVODMMVAYLETRLDWIHSSGMAEFTALYGDGALBEARLR 163
 DB 98 GALCVESVDKEMQVLSRIATWATYLDNHLEPWIQENGMDTFVELYGNNAAESRKGQ 157
 QY 164 E--GNMASVRYTLTGAVALGAL 183
 DB 158 ERFNRWFLTGMTVAGVLLGSL 179

RESULT 15
 ID Q99N35 PRELIMINARY; PRT; 217 AA.

AC Q99N35;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE B-cell leukemia/lymphoma x (Fragment).
 GN BCLX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Svj;
 RA Yang X.-F.; Cantor H.;
 RT "Novel cDNA structure and genomic organization of apoptosis regulatory
 RT gene Bcl-x-gamma";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF133282; AAK15455.1; -
 DR EMBL; AF133281; AAK15455.1; JOINED.
 DR HSSP; P53563; IAF3.
 DR GO; GO:0016020; Cmembrane; IEA.
 DR GO; GO:0016329; Fapoptosis regulator activity; IEA.
 DR GO; GO:0006915; Fapoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR002475; BCL2_FAMILY.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 FT NON_TER 1
 FT NON_TER 180
 SQ SEQUENCE 217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;

Query Match 39.7%; Score 401; DB 11; Length 217;
 Best Local Similarity 53.5%; Pred. No. 1.4e-27;
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEFEFRFRFTSDLAQLHVTGSAQORFTQVSDELFOGQPNMGRIVAFFVFG 103

DB 72 QALREAGDEFEFLRYRRAFSDLTSGQLHTPGTAYQSFEOYVNELFRDGVNMGRIVAFSFG 131
 QY 104 AALCAESVKNKEMEPVGVQVODMMVAYLETRLDWIHSSGMAEFTALYGDGALBEARLR 163
 DB 132 GALCVESVDKEMQVLSRIATWATYLDNHLEPWIQENGMDTFVDLYGNNAAESRKGQ 191
 QY 164 E--GNMASVRYTLTGAVALGAL 183
 DB 192 ERFNRWFLTGMTVAGVLLGSL 213

Search completed: March 25, 2004, 15:44:27
 Job time : 37 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: March 25, 2004, 15:36:20 ; Search time 14 Seconds
(without alignments)
1326.069 Million cell updates/sec

Title: US-09-155-327g-9
Perfect score: 1009
Sequence: 1 MATPASTPDRALVADPVGY.....LTGAVLGLVTVGAFPAASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	428.5	42.5	233	2	bcl-x long - mouse
2	427.5	42.4	233	2	apoptosis regulato
3	424.5	42.1	233	2	BCl-X protein - ra
4	423.5	42.0	233	2	transforming prote
5	414	41.0	232	2	transforming prote
6	411.5	40.8	239	1	transforming prote
7	411	40.7	236	2	BCl-2 - rat (fragm
8	406	40.2	236	2	Gene bcl-2 protein
9	405	40.1	236	1	transforming prote
10	404.5	40.1	233	2	BCl-X-Long - rat
11	402	39.8	236	2	B-cell lymphoma 2
12	378	37.5	190	2	apoptosis regulato
13	377.5	37.4	214	2	bcl-x transmembran
14	374.5	37.1	227	2	apoptosis regulato
15	356	35.3	216	2	transforming prote
16	348.5	34.5	199	1	transforming prote
17	345	34.2	205	1	transforming prote
18	277.5	27.5	154	2	gene bcl-2 protein
19	182	18.0	170	2	bcl-x short - mous
20	174	17.2	176	2	gene bcl-xshort pr
21	171	16.9	211	2	Bak protein - huma
22	168	16.7	211	2	cdh-2 protein - hu
23	158.5	15.7	192	2	bcl-2-associated p
24	154	15.3	192	2	bcl-2-associated p
25	151	15.0	261	2	apoptosis suppress
26	150.5	14.9	133	2	bcl-2-associated p
27	147.5	14.6	179	2	Bax-delta protein
28	147.5	14.6	218	2	bcl-2-associated p
29	147.5	14.6	218	2	bcl-2-associated p

30	142	14.1	177	2	S54778	NR-13 protein - qu
31	138.5	13.7	143	2	I38921	bcl-2-associated p
32	138	13.7	255	2	UC7567	Mcl-1a protein - z
33	116	11.5	175	2	I39055	Bcl-2 related - hu
34	116	11.5	350	2	A47476	BCL2 homolog MCL1
35	105	10.4	172	2	I49449	hemopoietic-specif
36	88	8.7	185	2	B83217	hypothetical prote
37	87	8.6	343	1	GNWYKV	genome polyprotein
38	86.5	8.6	301	2	T36534	probable lipase/es
39	86	8.5	270	2	A12598	dihydrodipicolinat
40	86	8.5	279	2	B97381	glutamate-ammonia
41	84.5	8.4	358	1	AUCQB	alanine-tRNA ligas
42	83.5	8.3	872	2	G98026	alanyl-tRNA synthe
43	83.5	8.3	872	2	H95160	genome polyprotein
44	83	8.2	3430	1	GNWYV	beta-amyloid-like
45	81.5	8.1	886	2	A32758	

ALIGNMENTS

RESULT 1
149056
bcl-x long - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C/Accession: I49056; S52866
R/Fang, W.; Rivard, J.U.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4368-4398, 1994
A/Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A/Reference number: I49055; WUID:95052604; PMID:7963517
A/Accession: I49056
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-233 <RES>
A/References: EMBL:U10101; NID:9506647; PIDN:AAA82173.1; PID:9506648
R/Kameaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
Submitted to the EMBL Data Library, November 1994
A/Description: IL-5 inhibits anti-IGM-induced apoptosis in an immature B cell line throu
A/Reference number: S52866
A/Accession: S52866
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-233 <RAM>
A/References: EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match	42.5%	Score 428.5;	DB 2;	Length 233;
Best Local Similarity	41.3%;	Pred. No. 2.2e-32;		
Matches	93;	Conservative	22;	Mismatches 57;
				Indels 53;
				Gaps 4;
QY	11	RATVADPVGYKLEOKGY	-----V	28
DB	6	RELVDVFLSYKLSQKGYSSQFSVDENETEAPEETEAARETPSALNGPSMHLADSPAV		65
QY	29	CGAGPEGEPAAD-----PLHOAMRAAGDFFETFRRTFSDLAOLHVTGSAQOQRT		80
DB	66	NGA-TGHSSSLDREVIYPMVAAYQALREAGDEFEELRYRAFDLTQSILHITGTAVQSPF		124
QY	81	QVSDLEIFQGGPWNKRLVAFVFGAALCAASVKNKEPELVGYQVODMMVALLEFRIDMTIS		140
DB	125	QVNNELFRGQVWNGRIVAFVFFSGALCVSVKXEMQVLSRASWATYIANHLEPWOE		184
QY	141	SGGMARFTLLYDGALEBARLRE--GNVASRYTVTGAVLGAAL		183
DB	185	NGGMDTFVDLYGNMRAABSRKGOERFRNRFITGMVAVGLLGS		229

RESULT 2

B47537
apoptosis regulator bcl-xl - human
N/Alternate names: bcl-2-related protein
N/Contains: apoptosis regulator bcl-xs

C:Species: Homo sapiens (man)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2003
C:Accession: B47537; C47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Turkka, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-2, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: B47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <BO>
A:Cross-references: GB:L20121; NID:9510900; PIDN:CAA80661.1; PID:9510901
A:Accession: C47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-69, 'G', '71-125, 189-233 <BO2>
A:Cross-references: GB:L20122; NID:9623236; PIDN:CAA80662.1; PID:9623237
C:Genetics:
A:Gene: GDB:BCI2L
A:Cross-references: GDB:228079
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; apoptosis
F.1-233/Product: apoptosis regulator bcl-XL #status predicted <MAT>
F.1-125, 189-233/Product: apoptosis regulator bcl-XS #status predicted <MA2>

Query Match 42.4%; Score 427.5; DB 2; Length 233;
Best Local Similarity 40.6%; Pred. No. 2.8e-32;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 PALVADPVGKLRQKGY-----VCGNPG---GEPPAA 39
DB 6 RELVDFLSTYLSQGYGWSQPSDVEENRTEAPEGTSEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQMRAAGDEFETRFRTFSDDLAAQLHVPFGSAQGFQ 81
DB 66 NGATTAHSSLDAREVTPMAAVKQALREAGDEFELRRIRAFSDLTLSQHLITPGTAYQSEFQ 125
QY 82 VSEDFQGGPNMGRIVAFVFGALCAESVKNEMEPVGVQVDMVAYLETRLDWTHSS 141
DB 126 VVNEIFRQGVNMGRIIVAFSFGALCVESVDKEMQVLSRIAMATYINDHLEPWIGEN 185
QY 142 GMAEFTALYDGALEEARLRE--GNMASVTVLTGAVALGAL 183
DB 186 GMDTFVDTLYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 3
S51761
BCL-X protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 26-Jul-2003
C:Accession: S51761; S51762
R:Michaels, T.M.
submitted to the EMBL Data Library, November 1994
A:Reference number: S51761
A:Accession: S51761
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MIC>
A:Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57886.1; PID:9607177
A:Experimental source: embryonic; brain
A:Accession: S51762
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125, 189-233 <MI2>
A:Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57887.1; PID:9607178
A:Experimental source: embryonic; brain
A>Note: smaller form due to splicing
C:Genetics:
A:Introns: 125/3
C:Superfamily: bcl apoptosis regulator, inhibitory type
Query Match 42.1%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 5.3e-32;
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;
QY 13 LVADPVGKLRQKGY-----VCG 30
DB 8 LVADPVGKLRQKGY-----VCG 30
QY 31 ACPGSPAD-----PLHQMRAAGDEFETRFRTFSDDLAAQLHVPFGSAQGFQ 82
DB 68 A-TGHSSTLDAREVTPMAAVKQALREAGDEFELRRIRAFSDLTLSQHLITPGTAYQSEFQ 126
QY 83 SEELFQGGPNMGRIVAFVFGALCAESVKNEMEPVGVQVDMVAYLETRLDWTHSS 142
DB 127 VVNEIFRQGVNMGRIIVAFSFGALCVESVDKEMQVLSRIAMATYINDHLEPWIGEN 186
QY 143 GMAEFTALYDGALEEARLRE--GNMASVTVLTGAVALGAL 183
DB 187 GMDTFVDTLYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 4
A37332
transforming protein (bcl-2-alpha) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
C:Accession: A37332; S35453
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: A37332
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-233 <EGU>
A:Cross-references: EMBL:D11381
C:Genetics:
A:Introns: 189/3
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.0%; Score 423.5; DB 2; Length 233;
Best Local Similarity 38.0%; Pred. No. 6.5e-32;
Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;
QY 9 DFRALVADPVGKLRQKGYCGAG-----FGEPPADP----- 41
DB 10 DNRRLVKTITHTKLSQGYGWSQPSDVEENRTEAPEGTSEMETPSAINGNPSWHLADSPAV 69
QY 42 -----PLHQMRAAGDEFETRFRTFSDDLAAQLHVPFGSAQGFQ 84
DB 70 AASEVPPAEGRLPAPPGVHALRQAGDEFERSRYQDFAQMSQHLITPFAHGRVAAVE 129
QY 85 ELFGGPNMGRIVAFVFGALCAESVKNEMEPVGVQVDMVAYLETRLDWTHSS 144
DB 130 ELFRDGVNMGRIIVAFSFGALCVESVDKEMQVLSRIAMATYINDHLEPWIGEN 189
QY 145 AEFTALYDGALEEARLRE--GNMASVTVLTGAVALGALVTVGAPFAS 193
DB 190 DAFVELYGN-----SKRPLDFSMISLTKTLLS-LVAVGACITVGAAYLGHK 233
RESULT 5
S24390
transforming protein (bcl-2) homolog - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 28-Jul-2003
C:Accession: S24390
R:Gazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
A:Reference number: S24390; MUID:92379084; PMID:1511008
A:Accession: S24390
A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-232 <CA6>
 A:Cross-references: EMBL:Z11961; NID:G62969; PIDD:CA78018.1; PID:G62970
 C:Superfamily: bcl apoptosis regulator, inhibitory type
 C:Keywords: mitochondrion; transmembrane protein

Query Match 41.0%; Score 414; DB 2; Length 232;
 Best Local Similarity 37.7%; Pred. No. 4,9e-31;
 Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

QY 9 DTRALVADPFVGYKLRQKGYCGAG-----PGSGPADP----- 41
 DB 10 DNRRLVWKYHYKLSQRGYEMDAGDVGAAPPGAAAPGIFSSQPGHTPHAPASRDVART 69
 QY 42 -----LHOAMRAAGDEFEFTRPRRTFSDLAAQLHVTTPGSAOQRTQVSD 85
 DB 70 LLVRCPRLRGCAAPGVHILALRQAGDEFSRRYQRFDAQMSQGLHPTFATGRFAVAYEE 129
 QY 86 LFQGGPNNRGLVAFPFVFGAALCAESYNKEMERLVGVQVDMMVAYLETFLADMIHSSGMA 145
 DB 130 LFRDGVNWRIVAFEFEGVWCVESVNRBMSPLVNDINATMMTEYLNRLHNMWIDQNGSD 189
 QY 146 EFTALVGDGALBEARLRREGNMAVSRTVLTGVALGALVTGAFPAASK 193
 DB 190 AFVELYGN-----PSMRPLPDFSWISLKTLLS-LVLVGACITTLGAYIGHK 232

RESULT 6

TVHUA1
 transforming protein bcl-2, splice form alpha - human

C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 28-Jul-2003
 C/Accession: C37332; A29409; S02452; A24428; A27622; B27622

R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A:Reference number: A57332; MUID:92375724; PMID:1508712

A:Accession: C37332

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-239 <EGU>

A>Note: this report is a correction

R/Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A>Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene

A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: A29409

A:Molecule type: mRNA

A:Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>

A:Cross-references: GB:M13994; NID:G179366; PIDD:AAA5183.1; PID:G179367

A>Note: this sequence has been corrected in reference A37332

R/Seto, M.; Jaeger, U.; Hockett, R.D.; Granger, W.; Bennett, S.; Goldman, P.; Korsmeyer

EMBO J. 7, 123-131, 1988

A>Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2

A:Reference number: S02452; MUID:88196071; PMID:2834197

A:Accession: S02452

A:Molecule type: mRNA

A:Residues: 1-239 <SET>

R/Cleary, M.L.; Smith, S.D.; Sklar, J.

Cell 47, 19-28, 1986

A>Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin

A:Reference number: A24428; MUID:87002488; PMID:2875799

A:Accession: A24428

A:Molecule type: mRNA

A:Residues: 1-58, 'T', 60-116, 'R', 118-239 <CLE>

A:Cross-references: GB:M1745; NID:G179370; PIDD:AAA5591.1; PID:G179371

R/Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.D.; Bakshi, A.

Oncogene Res. 2, 263-275, 1988

A>Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
 A:Reference number: A27622; MUID:88217344; PMID:3285301
 A:Accession: A27622
 A:Molecule type: mRNA
 A:Residues: 1-58, 'T', 60-239 <HUA>

A:Accession: B27622

A:Molecule type: DNA

A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA2>

A>Note: the sequence was determined from the germ-line gene

C/Comment: Constitutive expression of Bcl2 following t(14;18) chromosomal translocation

C/Genetics:

A:Gene: GDB:BCL2

A:Cross-references: GDB:119031; OMIM:151430

A:Map position: 18q21.3-18q21.3

C/Function:

A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl apoptosis regulator, inhibitory type

C/Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 40.8%; Score 411.5; DB 1; Length 239;
 Best Local Similarity 37.0%; Pred. No. 8,8e-31;
 Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

QY 9 DTRALVADPFVGYKLRQKGYCGAG-----PGSGPADP----- 35
 DB 10 DNRRLVWKYHYKLSQRGYEMDAGDVGAAPPGAAAPGIFSSQPGHTPHAPASRDVART 69
 QY 36 -----GPAADP-----LHOAMRAAGDEFEFTRPRRTFSDLAAQLHVTTPGSAOQ 78
 DB 70 SPLQTPAAGPAAAGPALSPVPVHILTRQAGDDFERRYRDFAEWMSQGLHPTFATGR 129
 QY 79 FTQVSDLEFQGGPNNRGLVAFPFVFGAALCAESYNKEMERLVGVQVDMMVAYLETFLADMI 138
 DB 130 FATVELEFEDGVNWRIVAFEFEGVWCVESVNRBMSPLVNDINATMMTEYLNRLHNMWIDQNGSD 189
 QY 139 HSSGMAEFPTALVGDGALBEARLRREGNMAVSRTVLTGVALGALVTGAFPAASK 193
 DB 190 QDNGMDAFVELYG-----PSMRPLPDFSWISLKTLLSL-LVGACITTLGAYIGHK 239

RESULT 7

167432
 BCL-2 - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 28-Jul-2003

C/Accession: 167432

R/Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.

Endocrinology 136, 232-241, 1995

A>Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin

constitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.

A:Reference number: 153295; MUID:95129487; PMID:7828536

A:Accession: 167432

A:Status: preliminary; translated from GB/EMBL/DDBL

A:Molecule type: mRNA

A:Residues: 1-236 <RES>

A:Cross-references: EMBL:U34964; NID:G1004378; PIDD:AAA77687.1; PID:G1004379

C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.7%; Score 411; DB 2; Length 236;
 Best Local Similarity 36.2%; Pred. No. 9,6e-31;
 Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADPFVGYKLRQKGY-----PGSGPADP----- 27
 DB 10 DNRRLVWKYHYKLSQRGYEMDAGDVGAAPPGAAAPGIFSSQPGHTPHAPASRDVART 69
 QY 28 -----VCGAGPGGPAADPLHOAMRAAGDEFEFTRPRRTFSDLAAQLHVTTPGSAOQRTQ 81
 DB 70 SPLRPVYANGPALSPVPVHILTRQAGDDFERRYRDFAEWMSQGLHPTFATGRFAT 129
 QY 82 VSDLEFQGGPNNRGLVAFPFVFGAALCAESYNKEMERLVGVQVDMMVAYLETFLADMIHSS 141
 DB 130 VVELEFEDGVNWRIVAFEFEGVWCVESVNRBMSPLVNDINATMMTEYLNRLHNMWIDQNGSD 189
 QY 142 GGMNPFALVGDGALBEARLRREGNMAVSRTVLTGVALGALVTGAFPAASK 193
 DB 190 GMDAFVELYG-----PSMRPLPDFSWISLKTLLSL-LVGACITTLGAYIGHK 236

A:Gene: bcl-2
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: B-cell lymphoma; ovary

Query Match 39.8%; Score 402; DB 2; Length 236;
Best Local Similarity 35.3%; Pred. No. 6.6e-30;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;

QY 9 PRLVADPVGKLRQKGY-----VCGAGPGE 27
DB 10 DNRREIMKXIKYKLSQKGSWQSDVEENRTAEDETSAINGNPSMHLADSPAV 69
QY 28 -----VCGAGPGEPAADPLHQAAMRAGDEPFRFRFTSPLAAQLHYTPGSAOQRTQ 81
DB 70 SPURPVIATGPTLSPVPVVLTLRRAGDDPSRRYRDPFAEMSQLHLPETARGPRAT 129
QY 82 VSDLEFQGGPNNGRLVAFVFGAALCAESVKNEMEPVGVQVQVMVAYLETRLADWHS 141
DB 130 VVEELFRDGVNNGRIYAFPSFGALCVESVDKEMQVLVSRISMTATYLNHLEPWIOE 189
QY 142 GGAWEFTALYGCALFEARLRGNWASVRYTLTGVALGALVTYGAFPAK 193
DB 190 GGMWAFVLYG---PSVRLPDPFWSLTKTLISLAL-VGACITTYIYGHK 236

RESULT 12

A47537
apoptosis regulator bcl-x - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 28-Jul-2003
C:Accession: A47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turk, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: A47537
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <BOI>
A:Cross-references: GB:I23110; GB:I20120; NID:9510899; PIDN:CAA80657.1; PID:9510899
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.5%; Score 378; DB 2; Length 190;
Best Local Similarity 43.8%; Pred. No. 8.6e-28;
Matches 81; Conservative 14; Mismatches 44; Indels 46; Gaps 3;

QY 11 PRLVADPVGKLRQKGY-----VCGAGPGE 37
DB 6 RELVIDFVSYKLSQKGSWQSDVEENRTAEDETSAINGNPSMHLADSPAV 65
QY 38 -----AADPLHQAAMRAGDEPFRFRFTSPLAAQLHYTPGSAOQRTQVSD 85
DB 66 VHRSSLEVEHEIVRASDPQALRDAGDEFLRYRRAFSDLTSLHTTPTGTAYSFGQVNE 125
QY 86 LQGGPNNGRLVAFVFGAALCAESVKNEMEPVGVQVQVMVAYLETRLADWHS 145
DB 126 LPHDGVNNGRIYAFPSFGALCVESVDKEMQVLVSRISMTATYLNHLEPWIOE 185
QY 146 EFTAL 150
DB 186 R-TAL 189

RESULT 13

I49057
bcl-x transmembrane deleted - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C:Accession: I49057
R:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49057; MUID:95052604; PMID:7963517

A:Accession: I49057

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-214 <RES>

A:Cross-references: EMBL:U10102; NID:9506649; PIDN:AAA82174.1; PID:9506650

C:Genetics:

A:Gene: bcl-x-long

C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.4%; Score 377.5; DB 2; Length 214;
Best Local Similarity 42.8%; Pred. No. 1.1e-27;
Matches 80; Conservative 16; Mismatches 40; Indels 51; Gaps 3;

QY 11 PRLVADPVGKLRQKGY-----V 28
DB 6 RELVIDFVSYKLSQKGSWQSDVEENRTAEDETSAINGNPSMHLADSPAV 65
QY 29 CGAGPGEPAAD-----PLHQAAMRAGDEPFRFRFTSPLAAQLHYTPGSAOQRT 80
DB 66 NGA-TGSSSIDAREVLPMAAVQALREAGDEFLRYRRAFSDLTSLHTTPTGTAQSFE 124
QY 81 QVSDLEFQGGPNNGRLVAFVFGAALCAESVKNEMEPVGVQVQVMVAYLETRLADWHS 140
DB 125 QVNVLEFRDGVNNGRIYAFPSFGALCVESVDKEMQVLVSRISMTATYLNHLEPWIOE 184
QY 141 SGWAEF 147
DB 185 NGWMTF 191

RESULT 14

JE0203
apoptosis regulator bcl-x isoform - human
N:Alternate names: h-bcl-xbeta
C:Species: Homo sapiens (man)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 28-Jul-2003
C:Accession: JE0203
R:Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A:Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A:Reference number: JE0203; MUID:98340865; PMID:9675101
A:Accession: JE0203
A:Molecule type: mRNA
A:Residues: 1-227 <BAN>
A:Cross-references: GB:U72398; NID:91622940; PIDN:AA817354.1; PID:91622941
C:Genetics:

A:Gene: bcl-x
A:Map position: 20
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.1%; Score 374.5; DB 2; Length 227;
Best Local Similarity 40.8%; Pred. No. 2.3e-27;
Matches 82; Conservative 18; Mismatches 50; Indels 51; Gaps 3;

QY 11 PRLVADPVGKLRQKGY-----V 28
DB 6 RELVIDFVSYKLSQKGSWQSDVEENRTAEDETSAINGNPSMHLADSPAV 65
QY 29 CGAGPGEPAAD-----PLHQAAMRAGDEPFRFRFTSPLAAQLHYTPGSAOQRT 80
DB 66 NGA-TGSSSIDAREVLPMAAVQALREAGDEFLRYRRAFSDLTSLHTTPTGTAQSFE 124
QY 81 QVSDLEFQGGPNNGRLVAFVFGAALCAESVKNEMEPVGVQVQVMVAYLETRLADWHS 140
DB 125 QVNVLEFRDGVNNGRIYAFPSFGALCVESVDKEMQVLVSRISMTATYLNHLEPWIOE 184
QY 141 SGWAEFTALYGCALFEAR 161
DB 185 NGWMTFVCPFSLASQR 205

RESULT 15

B37332

transforming protein (bcl-2-beta) - chicken

C;Species: Gallus gallus (chicken)

C:\Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003

C;Accession: B37332; S35452

R; Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A; Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
A; Reference number: A37333; PMID: 82375734; PMID: 1508712

A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: B37332

A;Accession: B37332
A;Status: published

A;Status: nucleic acid sequence not shown
A:Molecule type: DNA

A;Molecule type: DNA
A;Residues: 1-216 <EGIT>

A;Residues: 1-216 <BGU>

C:Superfamily: bcl apoptosis regulator, inhibi
A;Cross references: EMBL:D11381; EMBL:D11382
C:Superfamily: bcl apoptosis regulator, inhibi

c:superfamily: bcl apoptosis regulator, inhibitory type

Query Match	35.3%;	Score 356;	DB 2;	Length 216;
Best Local Similarity	38.4%;	Pred. No. 1.1e-25;		
Matches	71;	Conservative	21;	Mismatches 49;
				Indels 44;
				Gaps 2;

QY	9	DTRLVLVDFPGYKLRQGCAYCCAG	-----GEGGAADP-----	41
Db	10	DNRKIVLKYIHYLSQRGYDMAAGDR	RPVYPAPAPAPAPAPAAVLAAGASHHRRPEPSA	69
QY	42	-----LHQAMPAAGDEFEFRFRRT	PSLUAQLHTVPGSAQOOFTOVSD	84
Db	70	AASEVPAPAEGLRAPAPCGVHL	ALRQAGDEFSRRQRDFQAQSQGLHTLPFGAHGRFAVAE	129
QY	85	ELFPGGPNMGRLVAFFVFGAALCAES	VNKMMEBELVQGVQDDMVAVLLETRLADWTHSSGWM	144
Db	130	ELFEDGVMGRIVAFPEFGGVMCS	VNRMESPLVNLIATWTTLEYLNHNLNMQDNGWM	189
QY	145	AEPTTA	149	
Db	190	VRACA	194	

Search completed: March 25, 2004, 15:45:07
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 15:19:05 ; Search time 51 Seconds

(without alignments)
1069.248 Million cell updates/sec

Title: US-09-155-327g-9

Perfect score: 1009

Sequence: 1 NATPASTPTPTALVADPFGY.....LTGAVALGALVTGAFASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003ds:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1009	100.0	193	2	AA05531 Mouse Bcl
2	1005	99.6	193	2	AA061391 Rat bcl-Y
3	1005	99.6	193	2	AA073391 The rat b
4	1000	99.1	192	2	AA073393 Protein s
5	1000	99.1	193	2	AA05530 Human Bcl
6	1000	99.1	193	7	ADDA6742 Human Pro
7	995	98.6	193	2	AA061392 Human bcl
8	995	98.6	193	2	AA073392 The human
9	993	98.4	193	2	AA06047 Human bcl
10	993	98.4	193	2	AA05532 Human Bcl
11	990	98.1	192	2	AA073394 Mammalian
12	967.5	95.9	192	2	AA05533 Mouse Bcl
13	876	86.8	168	2	AA06048 Mouse bcl
14	814.5	75.2	190	5	AA018223 Human bcl
15	759	75.2	365	2	AA059884 Human act
16	759	75.2	365	5	AB039556 Human nov
17	759	75.2	365	6	AB034750 Fragment
18	432.5	42.7	411	4	AAU00219 Bcl-X1-DT
19	430.5	42.5	237	5	AB078480 Wild type
20	428.5	42.5	233	4	AB073303 Rat wild-
21	428.5	42.5	233	7	AD062921 Rat Prote
22	428.5	42.5	233	7	AD062491 Rat Prote
23	427.5	42.4	233	2	AA068887 Human thy
24	427.5	42.4	233	2	AA058821 Bcl-XL pr
25	427.5	42.4	233	2	AA015530 Human ant

26	427.5	42.4	233	3	AA069669 Human Bcl
27	427.5	42.4	233	3	AA063223 Bcl-x pol
28	427.5	42.4	233	4	AA050538 Human Bcl
29	427.5	42.4	233	4	AA064262 Human Bcl
30	427.5	42.4	233	4	AA047515 Protein e
31	427.5	42.4	233	7	AD062493 Human Pro
32	427.5	42.4	236	6	AB083558 ToLA-BCL
33	427.5	42.4	348	6	AB083557 ToLA-BCL
34	425	42.1	225	2	AA079396 "Deprenyl
35	424.5	42.1	233	4	AA073304 Mutant ra
36	415.5	41.2	239	4	AA064037 Human Bcl
37	414.5	41.1	152	6	AA079760 Bcl-XL, 4
38	412	40.8	236	5	AA076554 Murine Bc
39	412	40.8	236	5	AA076554 Murine Bc
40	411.5	40.8	239	2	AA067810 A human B
41	411.5	40.8	239	4	AA055130 Human Bcl
42	411.5	40.8	239	4	AA074127 Human Bcl
43	411.5	40.8	239	5	AB078479 Human Bcl
44	411.5	40.8	239	5	AB078478 Human Bcl
45	411.5	40.8	239	5	AA076553 Human Bcl

ALIGNMENTS

RESULT 1
AA05531
ID AA05531 standard; protein; 193 AA.
AC AA05531;
XX
XX
DT 05-JUL-1999 (first entry)
XX
XX
DE Mouse Bcl-w protein essential for spermatogenesis.
XX
XX
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
XX
OS Mus sp.
XX
XX
PN W09913710-A1.
XX
XX
PD 25-MAR-1999.
XX
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
XX
PR 16-SEP-1997; 97AU-00009228.
XX
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX
PI Cory S, Adams J, Print C, Gibson L, Koentgen F,
XX
XX
DR WPT; 1999-243890/20.
XX
XX
N-PSDB; AAX25133.
XX
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX
XX
PS Claim 2; Page 35; 52pp; English.
XX
XX
PS The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2
XX
XX
XX family which is widely expressed and which is essential for
XX
XX spermatogenesis. The invention relates generally to a method of treatment
XX
XX and to an animal model for the identification of molecules and genetic
XX
XX sequences useful for inducing or reducing fertility of male animals.
XX
XX Methods are provided for the treatment of infertility, or for reducing
XX
XX fertility, by modulating spermatogenesis. An animal model carries a
XX
XX mutation in at least one allele of the human or murine bcl-w gene (see
XX
XX AAX25132-35) or in a gene associated with bcl-w. Such animals have
XX
XX disorganised seminiferous tubules and are substantially infertile, but
XX
XX possess no other major abnormalities as determined by histological
XX
XX examination. They can be used to screen for therapeutic molecules
XX
XX including genetic sequences capable of inducing, enhancing or otherwise

CC facilitating spermatogenesis in animals, or which can induce infertility
 XX Sequence 193 AA;

Query Match 100.0%; Score 1009; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 7.4e-102;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEFETFRRT 60
 DB 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEFETFRRT 60
 QY 61 FSDLAAGLHVTGPSAQCRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNKEMLVVG 120
 DB 61 FSDLAAGLHVTGPSAQCRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNKEMLVVG 120
 QY 121 QVQDMWVAYLETRLADWIIHSSGMAEFTALYGDGALAEARLRREGNMAVRYTLTGAVALL 180
 DB 121 QVQDMWVAYLETRLADWIIHSSGMAEFTALYGDGALAEARLRREGNMAVRYTLTGAVALL 180
 QY 181 GALVTGAFPFASK 193
 DB 181 GALVTGAFPFASK 193

RESULT 2

AAW61391
 ID AAW61391 standard; protein; 193 AA.

XX AAW61391;
 AC
 XX 02-OCT-1998 (first entry)
 DT
 XX Rat bcl-y protein.
 DE
 XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
 KW
 XX Rattus sp.
 OS
 XX US5789201-A.
 PN
 XX 04-AUG-1998.
 PD
 XX 11-FEB-1997; 97US-00798897.
 PF
 XX 23-FEB-1996; 96US-0012201P.
 PR
 XX (COCE-) COCENSYS INC.
 PA
 XX Guastella J;
 PI
 XX WPI; 1998-446079/38.
 DR
 XX N-PSDB; AAV28333.
 XX
 PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
 PT recombinant protein for use in treating uncontrolled cell growth e.g.
 PT cancers.
 PT
 PS Example; Fig 3A; 27pp; English.
 XX
 CC The mammalian bcl-y protein is a member of the bcl-2 family, components
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity
 CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
 CC activity category. The recombinant protein may be used to prevent
 CC uncontrolled cell growth, either by its direct administration to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired
 XX
 XX Sequence 193 AA;

Query Match 99.6%; Score 1005; DB 2; Length 193;
 Best Local Similarity 99.5%; Pred. No. 2e-101;

Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEFETFRRT 60
 DB 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAMRAAGDEFETFRRT 60
 QY 61 FSDLAAGLHVTGPSAQCRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNKEMLVVG 120
 DB 61 FSDLAAGLHVTGPSAQCRFTQVSDELFOGGPNWGRVAFVFGAALCAESVNKEMLVVG 120
 QY 121 QVQDMWVAYLETRLADWIIHSSGMAEFTALYGDGALAEARLRREGNMAVRYTLTGAVALL 180
 DB 121 QVQDMWVAYLETRLADWIIHSSGMAEFTALYGDGALAEARLRREGNMAVRYTLTGAVALL 180
 QY 181 GALVTGAFPFASK 193
 DB 181 GALVTGAFPFASK 193

RESULT 3

AAW97391
 ID AAW97391 standard; protein; 193 AA.

XX AAW97391;
 AC
 XX 20-MAY-1999 (first entry)
 DT
 XX The rat bcl-y protein.
 DE
 XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 KW
 XX Rattus sp.
 OS
 XX US5883229-A.
 PN
 XX 16-MAR-1999.
 PD
 XX 25-NOV-1997; 97US-00978523.
 PF
 XX 23-FEB-1996; 96US-0012201P.
 PR
 XX 11-FEB-1997; 97US-00798897.
 XX
 PA (COCE-) COCENSYS INC.
 XX
 XX Guastella J;
 PI
 XX WPI; 1999-214150/18.
 DR
 XX N-PSDB; AAX15945.
 XX
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
 PT modulating programmed cell death.
 PT
 PS Disclosure; Col 15-18; 26pp; English.
 XX

XX The present sequence represents rat bcl-y protein (Rbcl-y). The
 CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
 CC - conditions where cells under go premature cell death as a result of
 CC triggers which may or may not be apparent. They may also be used in this
 CC way to develop cell lines which remain viable in culture for an extended

Rbcl-y and Hbcl-y proteins may be used to treat conditions associated

PS Claim 2; Page 33; 52pp; English.
XX
CC The present sequence is human Bcl-2, a pro-survival member of the Bcl-2

CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation is at least one allele of the human or murine bcl-w gene (see
CC AX25132-35) or in a gene associated with bcl-w. Such animals have
CC disorganised semiferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise
CC facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ Sequence 193 AA:

Query Match 99.1%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 7.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPPTRALVADPVGYKLRQKGYVCGAGGEGBPADPLHQMRAGDEFTFRRT 60
DB 1 MATPASPPTRALVADPVGYKLRQKGYVCGAGGEGBPADPLHQMRAGDEFTFRRT 60
QY 61 FSDLAQLHTVTPGSAQCRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVKNEMEPVVG 120
DB 61 FSDLAQLHTVTPGSAQCRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVKNEMEPVVG 120
QY 121 QVQDMWVAYLETRLADWHSGGMAEFTALYGDGALIEARLRREGNMAVSRTVLTGAVAL 180
DB 121 QVQDMWVAYLETRLADWHSGGMAEFTALYGDGALIEARLRREGNMAVSRTVLTGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 6
ADD46742
ID ADD46742 standard; protein; 193 AA.

XX AC ADD46742;

DT 29-JAN-2004 (first entry)

XX Human Protein Q92843, SEQ ID NO 12427.

DE Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

OS Homo sapiens.

XX WO2003016475-A2.

PN 27-FEB-2003.

XX 14-AUG-2002; 2002MO-US025765.

PF 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333447P.

XX (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Coeigan M;
XX WPI; 2003-268312/26.
XX GENBANK; Q92843.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIGO at
XX ftp.wigo.int/pub/published_pct_sequences.

SQ Sequence 193 AA:

Query Match 99.1%; Score 1000; DB 7; Length 193;
Best Local Similarity 99.0%; Pred. No. 7.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPPTRALVADPVGYKLRQKGYVCGAGGEGBPADPLHQMRAGDEFTFRRT 60
DB 1 MATPASPPTRALVADPVGYKLRQKGYVCGAGGEGBPADPLHQMRAGDEFTFRRT 60
QY 61 FSDLAQLHTVTPGSAQCRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVKNEMEPVVG 120
DB 61 FSDLAQLHTVTPGSAQCRFTQVSDELFOGSPNMGRLVAFVFGAALCAESVKNEMEPVVG 120
QY 121 QVQDMWVAYLETRLADWHSGGMAEFTALYGDGALIEARLRREGNMAVSRTVLTGAVAL 180
DB 121 QVQDMWVAYLETRLADWHSGGMAEFTALYGDGALIEARLRREGNMAVSRTVLTGAVAL 180
QY 181 GALVTVGAFPAASK 193
DB 181 GALVTVGAFPAASK 193

RESULT 7
AAW61392

ID AAW61392 standard; protein; 193 AA.

XX AAW61392;

DT 02-OCT-1998 (first entry)

DE Human bcl-y protein.

XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

OS Homo sapiens.

XX US5789201-A.

PN 04-AUG-1998.

XX 11-FEB-1997; 97US-00798897.

```

XX 23-FEB-1996; 96US-0012201P.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX MPI; 1998-446079/38.
XX N-PSDB; AAV28334.
XX
XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
XX recombinant protein for use in treating uncontrolled cell growth e.g.
XX cancers.
XX
XX Example; Column 17/18; 27bp; English.
XX
XX The mammalian bcl-y protein is a member of the bcl-2 family, components
XX in the cell death pathway. The bcl-2 family have both apoptotic activity
XX and the apoptosis blocking activity. bcl-y falls in the apoptosis
XX activity category. The recombinant protein may be used to prevent
XX uncontrolled cell growth, either by its direct administration to
XX recombinant genetic constructs to increase its expression in vivo. Also,
XX antisense constructs can be used in disorders where prevention of cell
XX death is desired
XX
XX Sequence 193 AA;
SQ
Query Match 98.6%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.5e-100;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASPTDTRALVADPFVGYKLRQKGYCGAGPEGPADPLHQAARAGDEFETFRRT 60
DB 1 MATPASPTDTRALVADPFVGYKLRQKGYCGAGPEGPADPLHQAARAGDEFETFRRT 60
QY 61 FSDLAQLHTVTPGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVNMKEPLVG 120
DB 61 FSDLAQLHTVTPGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVNMKEPLVG 120
QY 121 QVODMMVAVYLETFLADWTHSSGWAFFETALYGDALBEARLRBGNMASVRYTLTGAVAL 180
DB 121 QVODMMVAVYLETFLADWTHSSGWAFFETALYGDALBEARLRBGNMASVRYTLTGAVAL 180
QY 181 GALVTGGAFFASK 193
DB 181 GALVTGGAFFASK 193
Db 181 GALVTGGAFFASK 193
RESULT 8
AAW97392
ID AAW97392 standard; protein; 193 AA.
XX
XX AAW97392;
AC
XX
XX 20-MAY-1999 (first entry)
XX
XX The human bcl-y protein.
XX
XX Rat bcl-y protein; Hbcl-Y; human bcl-y protein; Hbcl-Y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death;
XX aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX premature cell death; cell death stimulator; prolonged cell life span;
XX Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
XX Homo sapiens.
XX
XX US5883229-A.
XX
XX 16-MAR-1999.
XX
XX 25-NOV-1997; 97US-00978523.

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XX 23-FEB-1996; 96US-0012201P.
XX 11-FEB-1997; 97US-00798897.
XX (COCE-) COCENSYS INC.
XX Guastella J;
XX MPI; 1999-214150/18.
XX N-PSDB; AAX15946.
XX
XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
XX modulating programmed cell death.
XX
XX Claim 1; Col 17-18; 26bp; English.
XX
XX The present sequence represents human bcl-y protein (Hbcl-Y). The
XX specification also describes rat bcl-y protein (Rbcl-Y). Rbcl-Y and Hbcl-
XX y are homologues of the bcl-2 protein thought to be involved in
XX programmed cell death (apoptosis and necrosis). Rbcl-Y and Hbcl-Y
XX proteins may be used to treat conditions associated with a disruption of
XX the cell death pathway. If they act as cell death inhibitors, they may be
XX used in therapies to treat subjects suffering from: strokes, head trauma,
XX Alzheimer's Disease, neural and muscular degenerative diseases
XX (especially multiple sclerosis), myocardial infarction, vitally induced
XX cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
XX - conditions where cells under go premature cell death as a result of
XX triggers which may or may not be apparent. They may also be used in this
XX way to develop cell lines which remain viable in culture for an extended
XX period. In contrast, if they act as cell death stimulators, Rbcl-Y and
XX Hbcl-Y may be used to treat conditions associated with prolonged cell
XX life span such as cancer (especially Kaposi's sarcoma and lung cancer)
XX and auto/hyperimmune diseases. They may also be used to cause cell death
XX in, and hence control, parasites
XX
XX Sequence 193 AA;
SQ
Query Match 98.6%; Score 995; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.5e-100;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASPTDTRALVADPFVGYKLRQKGYCGAGPEGPADPLHQAARAGDEFETFRRT 60
DB 1 MATPASPTDTRALVADPFVGYKLRQKGYCGAGPEGPADPLHQAARAGDEFETFRRT 60
QY 61 FSDLAQLHTVTPGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVNMKEPLVG 120
DB 61 FSDLAQLHTVTPGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVNMKEPLVG 120
QY 121 QVODMMVAVYLETFLADWTHSSGWAFFETALYGDALBEARLRBGNMASVRYTLTGAVAL 180
DB 121 QVODMMVAVYLETFLADWTHSSGWAFFETALYGDALBEARLRBGNMASVRYTLTGAVAL 180
QY 181 GALVTGGAFFASK 193
DB 181 GALVTGGAFFASK 193
Db 181 GALVTGGAFFASK 193
RESULT 9
AAW36047
ID AAW36047 standard; protein; 193 AA.
XX
XX AAW36047;
AC
XX
XX 22-APR-1998 (first entry)
XX
XX Human bcl-w protein.
XX
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX diagnosis; degenerative disease.
XX
XX Homo sapiens.
XX

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PN WO9735971-A1.
 XX 02-OCT-1997.
 PD 27-MAR-1997; 97WO-AU000199.
 XX 27-MAR-1996; 96AU-00008965.
 PR (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PA Cory S, Adams JM, Gibson LM, Holmgren SP;
 PI WPI; 1997-489635/45.
 DR N-PSDB; AAT96577.
 XX
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.
 PS
 XX Claim 6; Page 48; 86pp; English.
 CC This sequence represents a novel human protein, bcl-w, encoded by the bcl
 CC -2 gene family and extracted from an adult brain library. This gene
 CC promotes cell survival, so its modulation is useful in treatment of
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
 CC ischemia, human immunodeficiency virus infection or in cell transplants.
 CC up-regulation of the gene can also be used to modify cell lines cultured
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators
 SQ Sequence 193 AA;

Query Match 98.4%; Score 993; DB 2; Length 193;
 Best Local Similarity 97.9%; Pred. No. 4.2e-100;
 Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGEPADPLHQMRRAAGDEFEFRRT 60
 DB 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGGEGEPADPLHQMRRAAGDEFEFRRT 60
 QY 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGALCAESVNMKEPVLG 120
 DB 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGALCAESVNMKEPVLG 120
 QY 121 QVQDMWVAVLETRADVHSSGMAEFTALYDGALEEARLRREGWNASVRYTLTGAVAL 180
 DB 121 QVQDMWVAVLETRADVHSSGMAEFTALYDGALEEARLRREGWNASVRYTLTGAVAL 180
 QY 181 GALVTVGAFPAASK 193
 DB 181 GALVTVGAFPAASK 193

RESULT 10
 AAY05532
 ID AAY05532 standard; protein; 193 AA.
 XX
 AC AAY05532;
 XX
 AC 05-JUL-1999 (first entry)
 DT
 XX
 DE Human Bcl-w protein essential for spermatogenesis.
 XX
 KM Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
 KM animal model.
 XX
 OS Homo sapiens.
 XX
 PN WO99137710-A1.

PD 25-MAR-1999.
 XX
 XX 16-SEP-1998; 98WO-AU000764.
 PF
 XX 16-SEP-1997; 97AU-00009228.
 PR
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA
 PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
 DR WPI; 1999-243890/20.
 DR N-PSDB; AAX25134.
 XX
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS
 XX Disclosure; Page 37; 52pp; English.

CC The present sequence is described of a derivative of human Bcl-w (see
 CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation is at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganized seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility

SQ Sequence 193 AA;
 Query Match 98.4%; Score 993; DB 2; Length 193;
 Best Local Similarity 97.9%; Pred. No. 4.2e-100;
 Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGEPADPLHQMRRAAGDEFEFRRT 60
 DB 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGGEGEPADPLHQMRRAAGDEFEFRRT 60
 QY 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGALCAESVNMKEPVLG 120
 DB 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGALCAESVNMKEPVLG 120
 QY 121 QVQDMWVAVLETRADVHSSGMAEFTALYDGALEEARLRREGWNASVRYTLTGAVAL 180
 DB 121 QVQDMWVAVLETRADVHSSGMAEFTALYDGALEEARLRREGWNASVRYTLTGAVAL 180
 QY 181 GALVTVGAFPAASK 193
 DB 181 GALVTVGAFPAASK 193

RESULT 11
 AAW97394
 ID AAW97394 standard; protein; 192 AA.
 XX
 AC AAW97394;
 XX
 AC 20-MAY-1999 (first entry)
 DT
 XX
 DE Mammalian bcl-y protein.
 XX

KM Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KM multiple sclerosis; myocardial infarction; vitally induced cell death;
 KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KM premature cell death; cell death stimulator; prolonged cell life span;

KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX Mammalia.
OS US5893229-A.
PN 16-MAR-1999.
PD 25-NOV-1997; 97US-00978523.
PE 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX (COCE-) COCENSYS INC.
PA Guastella J;
PI WPI; 1999-214150/18.
XX DR Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
XX PT modulating programmed cell death.
XX PS Claim 2; Col 19-22; 26pp; English.
XX CC The present sequence represents a mammalian bcl-y protein. The
XX CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
XX CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
XX CC thought to be involved in programmed cell death (apoptosis and necrosis).
XX CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
XX CC with a disruption of the cell death pathway. If they act as cell death
XX CC inhibitors, they may be used in therapies to treat subjects suffering
XX CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
XX CC degenerative diseases (especially multiple sclerosis), myocardial
XX CC infarction, vitally induced cell death, aging, spinal cord injuries and
XX CC ankyrotic lateral sclerosis- conditions where cells under go premature
XX CC cell death as a result of triggers which may or may not be apparent. They
XX CC may also be used in this way to develop cell lines which remain viable in
XX CC culture for an extended period. In contrast, if they act as cell death
XX CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
XX CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
XX CC and lung cancer) and autoimmune diseases. They may also be used to
XX CC cause cell death in, and hence control, parasites
SQ Sequence 192 AA;
Query Match 98.4%; Score 990; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 8.8e-100;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 ATPASTPTDTRALVADPFVGYLRQKGYVCGAPGEGPADPLHOAMBAAGDEFTFRRTF 61
DB 1 ATPASAPDTALVEDPFVGYLRQKGYVCGAPGEGPADPLHOAMBAAGDEFTFRRTF 60
QY 62 SDLAAGLHTVPPGSAQGRFTQVSDDELFGCGPNMGRILVAFVFGAALCAESVNKMEPLVQ 121
DB 61 SDLAAGLHTVPPGSAQGRFTQVSDDELFGCGPNMGRILVAFVFGAALCAESVNKMEPLVQ 120
QY 122 VQDMWVAVYETRLADWTHSSGWAFFALYGDALBEARRLRGNMNASVTVLTGAVALG 181
DB 121 VQDMWVAVYETRLADWTHSSGWAFFALYGDALBEARRLRGNMNASVTVLTGAVALG 180
QY 182 ALVTGAFPFASK 193
DB 181 ALVTGAFPFASK 192

RESULT 12
AAV05533
ID AAV05533 standard; protein; 192 AA.
XX AAV05533;
XX 05-JUL-1999 (first entry)

XX DE Mouse Bcl-w protein derivative.
XX KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
XX KW animal model.
XX OS Mus sp.
XX PN WO9913710-A1.
XX PD 25-MAR-1999.
XX PF 16-SEP-1998; 98WO-AU000764.
XX PR 16-SEP-1997; 97AU-00009228.
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX PA Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX PI WPI; 1999-243890/20.
XX DR N-PSDB; AAX25135.
XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX PS protein associated with Bcl-w.
XX CC Disclosure; Page 39; 52pp; English.
XX CC The present sequence is described of a derivative of mouse Bcl-w (see
XX CC also AAV05531), a pro-survival member of the Bcl-2 family that is widely
XX CC expressed and which is essential for spermatogenesis. The derivative
XX CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates
XX CC generally to a method of treatment and to an animal model for the
XX CC identification of molecules and genetic sequences useful for inducing or
XX CC reducing fertility of male animals. Methods are provided for the
XX CC treatment of infertility, or for reducing fertility, by modulating
XX CC spermatogenesis. An animal model carries a mutation in at least one
XX CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
XX CC associated with Bcl-w. Such animals have disorganized seminiferous tubules
XX CC and are substantially infertile, but possess no other major abnormalities
XX CC as determined by histological examination. They can be used to screen for
XX CC therapeutic molecules including genetic sequences capable of inducing
XX CC enhancing or otherwise facilitating spermatogenesis in animals, or which
XX CC can induce infertility
SQ Sequence 192 AA;
Query Match 95.9%; Score 967.5; DB 2; Length 192;
Best Local Similarity 95.9%; Pred. No. 2.5e-97;
Matches 185; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
QY 1 MATPASTPTDTRALVADPFVGYLRQKGYVCGAPGEGPADPLHOAMBAAGDEFTFRRT 60
DB 1 MPTPASTPTDTRALVADPFVGYLRQKGYVCGAPGEGPADPLHOAMBAAGDEFTFRRT 60
QY 61 FSDLAAGLHTVPPGSAQGRFTQVSDDELFGCGPNMGRILVAFVFGAALCAESVNKMEPLVQ 120
DB 61 FSDLAAGLHTVPPGSAQGRFTQVSDDELFGCGPNMGRILVAFVFGAALCAESVNKMEPLVQ 120
QY 121 QVQDMWVAVYETRLADWTHSSGWAFFALYGDALBEARRLRGNMNASVTVLTGAVAL 180
DB 121 QVQDMWVAVYETRLADWTHSSGWAFFALYGDALBEARRLRGNMNASVTVLTGAVAL 179
QY 181 GALVTGAFPFASK 193
DB 180 GALVTGAFPFASK 192

RESULT 13
AAW36048
ID AAW36048 standard; protein; 168 AA.
XX AAW36048;
XX

XX 22-APR-1998 (first entry)
 XX Mouse bcl-w protein.
 XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 XX diagnosis; degenerative disease.
 KM Mus sp.
 XX WO9735971-A1.
 XX 02-OCT-1997.
 XX 27-MAR-1997; 97WO-AU000159.
 XX 27-MAR-1996; 96AU-00008965.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Cory S, Adams JM, Gibson LM, Holmgreen SP;
 XX WPI: 1997-489635/45.
 XX N-PSDB; AAT96578.
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.
 PS Claim 6; Page 50-51; 86pp; English.
 XX This sequence represents a novel protein, bcl-w, encoded by the mouse bcl
 CC -2 gene family. This gene promotes cell survival, so its modulation is
 CC useful in treatment of cancer or auto-immune diseases; degenerative
 CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
 CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
 CC or in cell transplants. Up-regulation of the gene can also be used to
 CC modify cell lines cultured in vivo, e.g. to develop new lines, to
 CC facilitate isolation of hybridomas and to increase survival of primary
 CC explants during genetic modification. It can be used to produce
 CC recombinant Bcl-w for therapy, diagnosis, antibody production or
 CC screening of potential modulators
 CC
 CC Sequence 168 AA;
 SQ
 Query Match 86.8%; Score 876; DB 2; Length 168;
 Best Local Similarity 97.0%; Pred. No. 2.2e-87;
 Matches 163; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPBGSPADPLHQAMRAAGDEFEFRFRPT 60
 DB 1 MPTPASTPTRALVADFGVYKLRQKGYVCGAGPBGSPADPLHQAMRAAGDEFEFRFRPT 60
 QY 61 FSDLAALHTVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGAALCAESVKNKEPVLVG 120
 DB 61 FSDLAALHTVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGAALCAESVKNKEPVLVG 120
 QY 121 QVQDMWVAVLETFLADWIHSSGMAEFTALYGDGALBEARLRREGNMA 168
 DB 121 QVQDMWVAVLETFLADWIHSSGMAEFTALYGDGALBEARLRREGNMA 168
 RESULT 14
 ID AAO18223 standard; protein; 190 AA.
 XX AAO18223;
 AC AAO18223;
 XX 18-SEP-2002 (first entry)
 DT Human Bcl-Rambo BHO domain related protein #4.
 XX Human Bcl-Rambo BHO domain related protein #4.
 DE Human; apoptotic signal transduction protein; Bcl-Rambo; BHO domain;
 KM

KM cancer; neurodegenerative disease; Alzheimer's disease; cytostatic;
 KM neurotropic; neuroprotective; antiparkinsonian; virucide; antiinflammatory;
 KM immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock;
 KM Parkinson's disease; muscular dystrophy; HIV; viral infection; hepatitis;
 KM graft versus host disease; autoimmune disease.
 XX Unidentified.
 OS
 XX WO200248353-A2.
 XX 20-JUN-2002.
 XX 12-DEC-2001; 2001WO-EP014597.
 XX 12-DEC-2000; 2000DE-01061766.
 XX 04-JAN-2001; 2001DE-01000280.
 XX (APOT-) APOTECHE RES & DEV LTD.
 XX Techopp J, Hofmann K;
 XX WPI: 2002-537627/57.
 DR New DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors and
 PT for identifying therapeutic modulators of Bcl-Rambo function.
 PT Disclosure; Fig 1; 61pp; German.
 PS
 XX The present invention provides the protein and coding sequences of the
 CC human Bcl-Rambo apoptotic transcription factor, particularly the BHO
 CC domain. The sequences are useful in the treatment of diseases caused by
 CC incorrectly regulated intracellular signal transduction, including
 CC cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's
 CC diseases), muscular dystrophy, viral infections (including human
 CC immunodeficiency virus), autoimmune disease, septic shock, graft versus
 CC host disease and acute hepatitis. The present sequence is a protein
 CC described in the exemplification of the invention
 CC
 CC Sequence 190 AA;
 SQ
 Query Match 80.7%; Score 814.5; DB 5; Length 190;
 Best Local Similarity 87.0%; Pred. No. 1.4e-80;
 Matches 168; Conservative 1; Mismatches 21; Indels 3; Gaps 3;
 QY 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPBGSPADPLHQAMRAAGDEFEFRFRPT 60
 DB 1 MATPASTPTRALVADFGVYKLRQKGYVCGAGPBGSPADPLHQAMRAAGDEFEFRFRPT 58
 QY 61 FSDLAALHTVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGAALCAESVKNKEPVLVG 120
 DB 59 FSDLAALHTVTPGSAQORFTQVSDLPFGGPNMGRVAFVFGAALCAESVKNKEPVLVG 118
 QY 121 QVQDMWVAVLETFLADWIHSSGMAEFTALYGDGALBEARLRREGNMA SVRTVLGVAL 180
 DB 119 QVQDMWVAVLETFLADWIHSSGMAEFTALYGDGALBEARLRREGNMA SVRTVLGVAL 177
 QY 181 GALVTYGAFFPAK 193
 DB 178 GALVTYGAFFPAK 190
 RESULT 15
 ID AAW59884 standard; protein; 365 AA.
 XX AAW59884;
 AC AAW59884;
 XX 20-NOV-1998 (first entry)
 DT Amino acid sequence of the cDNA clone Bcl-1-like (HAICH29).
 XX Bcl-1-like (HAICH29); chronic inflammatory disease; allergic reaction;
 DE immunological disorder; autoimmune disease; anti-infectious agent.
 KM

XX Homo sapiens.
 OS WO9831800-A2.
 PN 23-JUL-1998.
 PD 21-JAN-1998; 98MO-US000960.
 PF 21-JAN-1997; 97US-0034204P.
 PR 21-JAN-1997; 97US-0034205P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (AUCC-) AUCCLAND UNISERVICES LTD.
 XX Ni J, Rosen CA, Gentz RL, Feng P, Krissansen GW, Su JY;
 PI WPI; 1998-414099/35.
 DR N-PSDB; AAV41925.
 XX New isolated polynucleotides and encoded polypeptides - used to develop
 PT products for treating e.g. inflammatory diseases, infections,
 XX immunological disorders, autoimmune diseases, allergies or tumours.
 PS Claim 1; Fig 12A-12D; 120pp; English.
 CC This is the amino acid sequence of the cDNA clone Bcl-1-like (HAICH29),
 CC used in the method of the invention. The products of the clone can be
 CC used for treating conditions associated with abnormal expression of the
 CC polypeptides. They can be used for e.g. treating chronic inflammatory
 CC diseases, immunological disorders, autoimmune diseases, inflammatory
 CC diseases, various allergies, and as anti-infectious agents. The products
 CC can also be used for detection and diagnosis
 SQ Sequence 365 AA;

Query Match 75.2%; Score 759; DB 2; Length 365;
 Best Local Similarity 98.6%; Pred. No. 3.9e-74;
 Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTPTALVADPFVGYKLRQGYVCGAGPGGPAADPLHQAMRAAGDEPFTFRRT 60
 Db 1 MATPASAPPTRALVADPFVGYKLRQGYVCGAGPGGPAADPLHQAMRAAGDEPFTFRRT 60
 QY 61 FSDLAAGLHVTPGSAQCRFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEMEPVVG 120
 Db 61 FSDLAAGLHVTPGSAQCRFTQVSDLPFGGPNMGRVAFVFGALCAESVKNKEMEPVVG 120
 QY 121 QVQDMNVAVLETRLDADWIHSSGGW 144
 Db 121 QVQDMNVAVLETRLDADWIHSSGGW 144

Search completed: March 25, 2004, 15:42:29
 Job time : 52 secs